SEQUENCE LISTING

<110> Lanahan, Mike

<120> Self-processing Plants and Plant Parts

<130> 109846.317

<140> US 60/315,281
<141> 2001-08-27

<160> 112

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 436
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<213> Artificial Sequence

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Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr
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Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe
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Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly

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275 280 285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
290 295 300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305 310 315 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
325 330 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
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Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
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Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
370 375 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385 390 395 400
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<220>
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Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala Glu Val Trp
    50                  55                  60
Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro Asp Thr Ser
65                  70                  75                  80
Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val Ile Glu Ala
                85                  90                  95
Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu Phe Lys Val
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Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu Lys Ala Asp
        115                 120                 125
Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val Leu Ser Glu
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Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu Ile Ile Glu
145                 150                 155                 160
Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu Asp Asp Tyr
                165                 170                 175
Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu Lys Thr Ile
            180                 185                 190
Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val Leu Leu Phe
        195                 200                 205
Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn Met Glu Tyr
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Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp Leu Asp Gly
225                 230                 235                 240
Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile Arg Thr Thr
                245                 250                 255
Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln Glu Ser Ala
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Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu Asn Asp Arg
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Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr Glu Ile His
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Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Gly Pro Gly Gly Val
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Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr His Val His
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Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu Asp Lys Asp
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Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu Phe Met Val
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Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His Thr Arg Ile
385                 390                 395                 400
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Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His Gly Ile Gly
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Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile Gly Glu Leu
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Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg Ile Asp Lys
435 440 445
Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val Ile Ala Ser
450 455 460
Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val Thr Tyr Trp
465 470 475 480
Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln Met Gly Leu
485 490 495
Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu His Lys Ile
500 505 510
Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly Trp Gly Ala
515 520 525
Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His Val Ala Ala
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Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val Phe Asn Pro
545 550 555 560
Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu Thr Lys Ile
565 570 575
Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys Leu Ile Lys
580 585 590
Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala Ala Cys His
595 600 605
Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala Lys Ala Asp
610 615 620
Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala Gln Lys Leu
625 630 635 640
Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe Leu His Gly
645 650 655
Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn Ser Tyr Asn
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Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys Leu Gln Phe
675 680 685
Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu Arg Lys Glu
690 695 700
His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys Lys His Leu
705 710 715 720
Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met Leu Lys Asp
725 730 735
His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile Tyr Asn Gly
740 745 750
Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys Trp Asn Val
755 760 765
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Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu Tyr Arg Glu
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<213> Artificial Sequence

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<223> synthetic

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<212> PRT
<213> Sulfolobus solfataricus

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Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile Val Gln Gln
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Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys Glu His Ile

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Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys Tyr Gln Asp
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Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys Asp Gly Val
            100                 105                 110
Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile Phe Asp Val
        115                 120                 125
Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro Glu Asp Ser
    130                 135                 140
Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp Val Leu Glu
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Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro Met Trp Ala
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Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln Asp Lys Val
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Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg Val Ala Gly
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Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu Phe Thr Trp
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His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp Glu Leu His
225                 230                 235                 240
Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly Ile Arg Val
                245                 250                 255
Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys Phe Cys Glu
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        275                 280                 285
Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp Trp Ala Gly
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Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln Leu Val Leu
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Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp Ile Gly Gly
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Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr Arg Ser His
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Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu Pro Asp Tyr
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Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro Arg Gly Lys
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            580                 585                 590
Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly Ser Ile Ile
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Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr Ser Phe Lys
    610                 615                 620
Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu Ile Lys Phe
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Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser Glu Lys Pro
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Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln Val Glu Lys
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<212> DNA
<213> Sulfolobus solfataricus

<400> 6

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<210> 8
<211> 606
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 8

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Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg Thr
        35                  40                  45
Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg Gly
    50                  55                  60
Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Met Asn Val
65                  70                  75                  80
Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu
                85                  90                  95
Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His
            100                 105                 110
Arg Val Met Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp
        115                 120                 125
Asp Thr Ser Val Val Ser Glu Ile Lys Met Gly Asp Gly Tyr Glu Thr
    130                 135                 140
Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val
145                 150                 155                 160
Asp His Pro Leu Phe Leu Glu Arg Val Trp Gly Lys Thr Glu Glu Lys
                165                 170                 175
Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln Leu Arg
            180                 185                 190
Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Ser
        195                 200                 205
Leu Asn Asn Asn Pro Tyr Phe Ser Gly Pro Tyr Gly Glu Asp Val Val
    210                 215                 220
Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys
225                 230                 235                 240
Ser Asn Tyr Gln Ser His Gly Ile Tyr Arg Asp Ala Lys Thr Ala Phe
                245                 250                 255
Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
            260                 265                 270
Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
        275                 280                 285
Asp Gly Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys
    290                 295                 300
Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr
305                 310                 315                 320
Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn
                325                 330                 335
Ile Met Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val
            340                 345                 350
Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp
        355                 360                 365
Val Ser Thr Ala Val Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln
    370                 375                 380
Ala Glu Val Gly Leu Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe
385                 390                 395                 400
Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala
                405                 410                 415
Ile Pro Gln Leu Met Glu Met Val Glu Asp Val Gln Ile Val Leu Leu
            420                 425                 430
Gly Thr Gly Lys Lys Lys Phe Glu Arg Met Leu Met Ser Ala Glu Glu
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Lys Phe Pro Gly Lys Val Arg Ala Val Val Lys Phe Asn Ala Ala Leu
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    450                 455                 460
Ala His His Ile Met Ala Gly Ala Asp Val Leu Ala Val Thr Ser Arg
465                 470                 475                 480
Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln Gly Met Arg Tyr Gly Thr
                485                 490                 495
Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu Val Asp Thr Ile Ile Glu
            500                 505                 510
Gly Lys Thr Gly Phe His Met Gly Arg Leu Ser Val Asp Cys Asn Val
        515                 520                 525
Val Glu Pro Ala Asp Val Lys Lys Val Ala Thr Thr Leu Gln Arg Ala
    530                 535                 540
Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val Arg Asn Cys
545                 550                 555                 560
Met Ile Gln Asp Leu Ser Trp Lys Gly Pro Ala Lys Asn Trp Glu Asn
                565                 570                 575
Val Leu Leu Ser Leu Gly Val Ala Gly Gly Glu Pro Gly Val Glu Gly
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Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala Ala Pro
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<210> 9
<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 9

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aacccgttcg tcggcgacta cacctggacg gacttctcca aggtcgcctc cggcaagtac 420
accgccaact acctcgactt ccaccccaac gagctgcacg cgggcgactc cggcacgttc 480
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caggagtcct acgcggccta cctgcgctcc atcggcatcg acgcgtggcg cttcgactac 600
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ccc 2223

<210> 10
<211> 741
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 10

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			20					25					30		
Gln	Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile
		35					40					45			
Pro	Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp
	50					55					60				
Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val
65					70					75					80
Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr
				85					90					95	
Ala	His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His
			100					105					110		
Arg	Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp	Tyr	Thr
		115					120					125			
Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr
	130					135					140				
Leu	Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe
145					150					155					160
Gly	Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp
				165					170					175	
Leu	Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly
			180					185					190		
Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val
		195					200					205			
Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr
	210					215					220				
Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly
225					230					235					240
Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe
				245					250					255	
Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly
			260					265					270		
Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn
		275					280					285			
His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile
	290					295					300				

Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305 310 315 320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
325 330 335
Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
340 345 350
Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
355 360 365
Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
370 375 380
Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
385 390 395 400
Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
405 410 415
Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
420 425 430
Cys Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val
435 440 445
Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala
450 455 460
Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly
465 470 475 480
Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys
485 490 495
Tyr Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala
500 505 510
Leu Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg
515 520 525
Asn Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly
530 535 540
Pro Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu
545 550 555 560
Asp Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg
565 570 575
Met Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val
580 585 590
Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
595 600 605
Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu
610 615 620
Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
625 630 635 640
Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
645 650 655
Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
660 665 670
Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
675 680 685
Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
690 695 700
Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
705 710 715 720
Gly Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu
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Asn Val Ala Ala Pro
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<210> 11
<211> 1515
<212> DNA
<213> Zea mays

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cagctcagaa aaaagttatc tatgaaaggt ttcatgtgta ccgtgggaaa tgagaaatgt 180
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tcaacacaca gttgtctgct ttatgatggc atctccaccc aggcacccac catcacctat 420
ctctcgtgcc tgtttatttt cttgcccttt ctgatcataa aaaaacatta agagtttgca 480
aacatgcata ggcatatcaa tatgctcatt tattaatttg ctagcagatc atcttcctac 540
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ccaatgcatc ttcattaaat gtgaatttca gaaaggaagt aggaacctat gagagtattt 660
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ttcagtttgg tcataagatg tcatattaaa gggcaaacat atattcaatg ttcaattcat 1440
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tagtagttgg aggag 1515

<210> 12
<211> 673
<212> DNA
<213> Zea mays

<400> 12
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aattgcacgt caagggtatt gggtaagaaa caatcaaaca aatcctctct gtgtgcaaag 180
aaacacggtg agtcatgccg agatcatact catctgatat acatgcttac agctcacaag 240
acattacaaa caactcatat tgcattacaa agatcgtttc atgaaaaata aaataggccg 300
gacaggacaa aaatccttga cgtgtaaagt aaatttacaa caaaaaaaaa gccatatgtc 360
aagctaaatc taattcgttt tacgtagatc aacaacctgt agaaggcaac aaaactgagc 420
cacgcagaag tacagaatga ttccagatga accatcgacg tgctacgtaa agagagtgac 480
gagtcatata catttggcaa gaaaccatga agctgcctac agccgtctcg gtggcataag 540
aacacaagaa attgtgttaa ttaatcaaag ctataaataa cgctcgcatg cctgtgcact 600
tctccatcac caccactggg tcttcagacc attagcttta tctactccag agcgcagaag 660
aacccgatcg aca 673

<210> 13
<211> 454
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 13

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            20                  25                  30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
        35                  40                  45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
    50                  55                  60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65                  70                  75                  80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
                85                  90                  95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
            100                 105                 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
        115                 120                 125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
    130                 135                 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145                 150                 155                 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
                165                 170                 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
            180                 185                 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
        195                 200                 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
    210                 215                 220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225                 230                 235                 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
                245                 250                 255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
            260                 265                 270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
        275                 280                 285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
    290                 295                 300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305                 310                 315                 320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
                325                 330                 335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
            340                 345                 350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
        355                 360                 365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
    370                 375                 380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385                 390                 395                 400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
                405                 410                 415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
            420                 425                 430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
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435 440 445
Ser Tyr Cys Gly Val Gly
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<210> 14
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 14
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Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
35 40 45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50 55 60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65 70 75 80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85 90 95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100 105 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115 120 125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130 135 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145 150 155 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165 170 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180 185 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195 200 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210 215 220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225 230 235 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245 250 255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260 265 270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275 280 285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290 295 300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305 310 315 320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325 330 335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340 345 350

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Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
          355                 360                 365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
      370                 375                 380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385                 390                 395                 400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
                405                 410                 415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
            420                 425                 430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
          435                 440                 445
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
      450                 455                 460
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<210> 15
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 15

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Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1               5                  10                  15
Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
            20                  25                  30
Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
        35                  40                  45
Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
    50                  55                  60
Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65                  70                  75                  80
Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe
                85                  90                  95
Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
            100                 105                 110
Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
        115                 120                 125
Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
    130                 135                 140
Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
145                 150                 155                 160
Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
                165                 170                 175
His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
            180                 185                 190
Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
        195                 200                 205
Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
    210                 215                 220
Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
225                 230                 235                 240
Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
                245                 250                 255
Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
```

260 265 270
Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
275 280 285
Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
290 295 300
Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
305 310 315 320
Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
325 330 335
Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
340 345 350
Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
355 360 365
Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
370 375 380
Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
385 390 395 400
Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
405 410 415
Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
420 425 430
Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
435 440 445
Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
450 455 460
Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
465 470 475 480
Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
485 490 495
Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
500 505 510
Gly Val Gly Thr Ser Ile
515

<210> 16
<211> 820
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 16
Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1 5 10 15
Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20 25 30
Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35 40 45
Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50 55 60
Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65 70 75 80
Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe
85 90 95
Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
100 105 110

```
Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
        115                 120                 125
Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
    130                 135                 140
Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
145                 150                 155                 160
Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
                165                 170                 175
His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
            180                 185                 190
Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
        195                 200                 205
Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
    210                 215                 220
Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
225                 230                 235                 240
Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
                245                 250                 255
Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
            260                 265                 270
Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
        275                 280                 285
Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
    290                 295                 300
Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
305                 310                 315                 320
Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
                325                 330                 335
Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
            340                 345                 350
Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
        355                 360                 365
Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
    370                 375                 380
Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
385                 390                 395                 400
Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
                405                 410                 415
Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
            420                 425                 430
Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
        435                 440                 445
Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
    450                 455                 460
Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
465                 470                 475                 480
Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
                485                 490                 495
Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
            500                 505                 510
Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val Leu
        515                 520                 525
Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg
    530                 535                 540
Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly Ile
545                 550                 555                 560
Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr
                565                 570                 575
```

```
Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala Leu
                580                 585                 590
Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg Asn
            595                 600                 605
Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro
        610                 615                 620
Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu Asp
625                 630                 635                 640
Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg Met
                645                 650                 655
Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val Val
            660                 665                 670
Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp Val
        675                 680                 685
Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln
    690                 695                 700
Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu
705                 710                 715                 720
Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu
                725                 730                 735
Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala
            740                 745                 750
Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu
        755                 760                 765
Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly Pro
    770                 775                 780
Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly
785                 790                 795                 800
Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn
                805                 810                 815
Val Ala Ala Pro
            820
```

<210> 17
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 17
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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1               5                  10                  15
Ala Thr Ser
```

<210> 18
<211> 444
<212> PRT
<213> Thermotoga maritima

<400> 18
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Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys
 1               5                  10                  15
Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val
```

```
                20                  25                  30
Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe
            35                  40                  45
Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
        50                  55                  60
Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe
65                  70                  75                  80
Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
                85                  90                  95
Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
            100                 105                 110
Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
        115                 120                 125
Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
    130                 135                 140
Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
145                 150                 155                 160
Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
                165                 170                 175
Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
            180                 185                 190
Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn
        195                 200                 205
Leu Ala Arg Phe Leu Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly
    210                 215                 220
Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys
225                 230                 235                 240
His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn
                245                 250                 255
His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala
            260                 265                 270
Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile
        275                 280                 285
Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu
    290                 295                 300
Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Ile Tyr Asp Thr Thr Leu
305                 310                 315                 320
Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu
                325                 330                 335
Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu
            340                 345                 350
Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys
        355                 360                 365
Ile Ala Tyr Lys Leu Ala Lys Asp Gly Val Phe Asp Lys Phe Ile Glu
    370                 375                 380
Glu Lys Tyr Arg Ser Phe Lys Glu Gly Ile Gly Lys Glu Ile Val Glu
385                 390                 395                 400
Gly Lys Thr Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu
                405                 410                 415
Asp Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Leu
            420                 425                 430
Asn Ser Tyr Ile Val Lys Thr Ile Ala Glu Leu Arg
        435                 440
```

<210> 19
<211> 1335
<212> DNA

<213> Thermotoga maritima

<400> 19
atggccgagt tcttcccgga gatcccgaag atccagttcg agggcaagga gtccaccaac 60
ccgctcgcct tccgcttcta cgacccgaac gaggtgatcg acggcaagcc gctcaaggac 120
cacctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgacccgttc 180
ggcgacccga ccgccgagcg cccgtggaac cgcttctccg acccgatgga caaggccttc 240
gcccgcgtgg acgccctctt cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgcg acatcgcccc ggagggcaag accctccgcg agaccaacaa gatcctcgac 360
aaggtggtgg agcgcatcaa ggagcgcatg aaggactcca acgtgaagct cctctggggc 420
accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacgccgc cgcccaggtg aagaaggccc tggagatcac caaggagctg 540
ggcggcgagg gctacgtgtt ctggggcggc cgcgagggct acgagaccct cctcaacacc 600
gacctcggcc tggagctgga gaacctcgcc cgcttcctcc gcatggccgt ggagtacgcc 660
aagaagatcg gcttcaccgg ccagttcctc atcgagccga agccgaagga gccgaccaag 720
caccagtacg acttcgacgt ggccaccgcc tacgccttcc tcaagaacca cggcctcgac 780
gagtacttca agttcaacat cgaggccaac cacgccaccc tcgccggcca caccttccag 840
cacgagctgc gcatggcccg catcctcggc aagctcggct ccatcgacgc caaccagggc 900
gacctcctcc tcggctggga caccgaccag ttcccgacca acatctacga caccaccctc 960
gccatgtacg aggtgatcaa ggccggcggc ttcaccaagg gcggcctcaa cttcgacgcc 1020
aaggtgcgcc gcgcctccta caaggtggag gacctcttca tcggccacat cgccggcatg 1080
gacaccttcg ccctcggctt caagatcgcc tacaagctcg ccaaggacgg cgtgttcgac 1140
aagttcatcg aggagaagta ccgctccttc aaggagggca tcggcaagga gatcgtggag 1200
ggcaagaccg acttcgagaa gctggaggag tacatcatcg acaaggagga catcgagctg 1260
ccgtccggca agcaggagta cctggagtcc ctcctcaact cctacatcgt gaagaccatc 1320
gccgagctgc gctga 1335

<210> 20
<211> 444
<212> PRT
<213> Thermotoga neapolitana

<400> 20
Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys
1 5 10 15
Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile
20 25 30
Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe
35 40 45
Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
50 55 60
Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe
65 70 75 80
Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
85 90 95
Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
100 105 110
Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
115 120 125
Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
130 135 140
Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
145 150 155 160
Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
165 170 175
Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
180 185 190
Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn

```
        195                 200                 205
Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly
    210                 215                 220
Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys
225                 230                 235                 240
His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser
                245                 250                 255
His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala
            260                 265                 270
Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile
        275                 280                 285
Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu
    290                 295                 300
Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu
305                 310                 315                 320
Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu
                325                 330                 335
Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu
            340                 345                 350
Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys
        355                 360                 365
Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu
    370                 375                 380
Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu
385                 390                 395                 400
Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu
                405                 410                 415
Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile
            420                 425                 430
Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
        435                 440
```

<210> 21
<211> 1335
<212> DNA
<213> Thermotoga neapolitana

<400> 21
atggccgagt tcttcccgga gatcccgaag gtgcagttcg agggcaagga gtccaccaac 60
ccgctcgcct tcaagttcta cgacccggag gagatcatcg acggcaagcc gctcaaggac 120
cacctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgacccgttc 180
ggcgacccga ccgccgaccg cccgtggaac cgctacaccg acccgatgga caaggccttc 240
gcccgcgtgg acgccctctt cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgcg acatcgcccc ggagggcaag accctccgcg agaccaacaa gatcctcgac 360
aaggtggtgg agcgcatcaa ggagcgcatg aaggactcca acgtgaagct cctctggggc 420
accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacgccgc cgcccaggtg aagaaggccc tggagatcac caaggagctg 540
ggcggcgagg gctacgtgtt ctggggcggc cgcgagggct acgagaccct cctcaacacc 600
gacctcggct tcgagctgga gaacctcgcc cgcttcctcc gcatggccgt ggactacgcc 660
aagcgcatcg gcttcaccgg ccagttcctc atcgagccga agccgaagga gccgaccaag 720
caccagtacg acttcgacgt ggccaccgcc tacgccttcc tcaagtccca cggcctcgac 780
gagtacttca agttcaacat cgaggccaac cacgccaccc tcgccggcca caccttccag 840
cacgagctgc gcatggcccg catcctcggc aagctcggct ccatcgacgc caaccagggc 900
gacctcctcc tcggctggga caccgaccag ttcccgacca acgtgtacga caccacctc 960
gccatgtacg aggtgatcaa ggccggcggc ttcaccaagg gcggcctcaa cttcgacgcc 1020
aaggtgcgcc gcgcctccta caaggtggag gacctcttca tcggccacat cgccggcatg 1080
gacaccttcg ccctcggctt caaggtggcc tacaagctcg tgaaggacgg cgtgctcgac 1140

aagttcatcg aggagaagta ccgctccttc cgcgagggca tcggccgcga catcgtggag 1200
ggcaaggtgg acttcgagaa gctggaggag tacatcatcg acaaggagac catcgagctg 1260
ccgtccggca agcaggagta cctggagtcc ctcatcaact cctacatcgt gaagaccatc 1320
ctggagctgc gctga 1335

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 22
agcgaattca tggcggctct ggccacgt 28

<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 23
agctaagctt cagggcgcgg ccacgttct 29

<210> 24
<211> 825
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 24

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ala	Ser
1				5				10						15	
Ala	Thr	Ser	Ala	Gly	His	Trp	Tyr	Lys	His	Gln	Arg	Ala	Tyr	Gln	Phe
			20					25					30		
Thr	Gly	Glu	Asp	Asp	Phe	Gly	Lys	Val	Ala	Val	Val	Lys	Leu	Pro	Met
		35					40					45			
Asp	Leu	Thr	Lys	Val	Gly	Ile	Ile	Val	Arg	Leu	Asn	Glu	Trp	Gln	Ala
	50					55					60				
Lys	Asp	Val	Ala	Lys	Asp	Arg	Phe	Ile	Glu	Ile	Lys	Asp	Gly	Lys	Ala
65					70					75					80
Glu	Val	Trp	Ile	Leu	Gln	Gly	Val	Glu	Glu	Ile	Phe	Tyr	Glu	Lys	Pro
				85					90					95	
Asp	Thr	Ser	Pro	Arg	Ile	Phe	Phe	Ala	Gln	Ala	Arg	Ser	Asn	Lys	Val
			100					105					110		
Ile	Glu	Ala	Phe	Leu	Thr	Asn	Pro	Val	Asp	Thr	Lys	Lys	Lys	Glu	Leu
		115					120					125			
Phe	Lys	Val	Thr	Val	Asp	Gly	Lys	Glu	Ile	Pro	Val	Ser	Arg	Val	Glu
	130					135					140				
Lys	Ala	Asp	Pro	Thr	Asp	Ile	Asp	Val	Thr	Asn	Tyr	Val	Arg	Ile	Val
145					150					155					160
Leu	Ser	Glu	Ser	Leu	Lys	Glu	Glu	Asp	Leu	Arg	Lys	Asp	Val	Glu	Leu
				165					170					175	

Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
180 185 190
Asp Asp Tyr Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
195 200 205
Lys Thr Ile Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val
210 215 220
Leu Leu Phe Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn
225 230 235 240
Met Glu Tyr Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp
245 250 255
Leu Asp Gly Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile
260 265 270
Arg Thr Thr Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln
275 280 285
Glu Ser Ala Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu
290 295 300
Asn Asp Arg Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr
305 310 315 320
Glu Ile His Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys
325 330 335
Asn Lys Gly Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Ala Pro
340 345 350
Gly Gly Val Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr
355 360 365
His Val His Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu
370 375 380
Asp Lys Asp Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu
385 390 395 400
Phe Met Val Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His
405 410 415
Thr Arg Ile Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His
420 425 430
Gly Ile Gly Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile
435 440 445
Gly Glu Leu Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg
450 455 460
Ile Asp Lys Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val
465 470 475 480
Ile Ala Ser Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val
485 490 495
Thr Tyr Trp Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln
500 505 510
Met Gly Leu Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu
515 520 525
His Lys Ile Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly
530 535 540
Trp Gly Ala Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His
545 550 555 560
Val Ala Ala Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val
565 570 575
Phe Asn Pro Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu
580 585 590
Thr Lys Ile Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys
595 600 605
Leu Ile Lys Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala
610 615 620
Ala Cys His Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala
625 630 635 640

Lys Ala Asp Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala
645 650 655
Gln Lys Leu Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe
660 665 670
Leu His Gly Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn
675 680 685
Ser Tyr Asn Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys
690 695 700
Leu Gln Phe Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu
705 710 715 720
Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys
725 730 735
Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met
740 745 750
Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile
755 760 765
Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys
770 775 780
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
785 790 795 800
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu
805 810 815
Tyr Arg Glu Ser Glu Lys Asp Glu Leu
820 825

<210> 25
<211> 2478
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 25
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ggccactggt acaagcacca gcgcgcctac cagttcaccg gcgaggacga cttcgggaag 120
gtggccgtgg tgaagctccc gatggacctc accaaggtgg gcatcatcgt gcgcctcaac 180
gagtggcagg cgaaggacgt ggccaaggac cgcttcatcg agatcaagga cggcaaggcc 240
gaggtgtgga tactccaggg cgtggaggag atcttctacg agaagccgga cacctccccg 300
cgcatcttct tcgcccaggc ccgctccaac aaggtgatcg aggccttcct caccaacccg 360
gtggacacca agaagaagga gctgttcaag gtgaccgtcg acggcaagga gatcccggtg 420
tcccgcgtgg agaaggccga cccgaccgac atcgacgtga ccaactacgt gcgcatcgtg 480
ctctccgagt ccctcaagga ggaggacctc cgcaaggacg tggagctgat catcgagggc 540
tacaagccgg cccgcgtgat catgatggag atcctcgacg actactacta cgacggcgag 600
ctgggggcgg tgtactcccc ggagaagacc atcttccgcg tgtggtcccc ggtgtccaag 660
tgggtgaagg tgctcctctt caagaacggc gaggacaccg agccgtacca ggtggtgaac 720
atggagtaca agggcaacgg cgtgtgggag gccgtggtgg agggcgacct cgacggcgtg 780
ttctacctct accagctgga gaactacggc aagatccgca ccaccgtgga cccgtactcc 840
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gagggctggg agaacgaccg cggcccgaag atcgagggct acgaggacgc catcatctac 960
gagatccaca tcgccgacat caccggcctg gagaactccg gcgtgaagaa caagggcctc 1020
tacctcggcc tcaccgagga gaacaccaag gccccgggcg gcgtgaccac cggcctctcc 1080
cacctcgtgg agctgggcgt gacccacgtg cacatcctcc cgttcttcga cttctacacc 1140
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gaggtgaagg agatggtgaa ggccctccac aagcacggca tcggcgtgat catggacatg 1320
gtgttcccgc acacctacgg catcggcgag ctgtccgcct tcgaccagac cgtgccgtac 1380

tacttctacc gcatcgacaa gaccggcgcc tacctcaacg agtccggctg cggcaacgtg 1440
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aaggagtacc acatcgacgg cttccgcttc gaccagatgg gcctcatcga caagaagacc 1560
atgctggagg tggagcgcgc cctccacaag atcgacccga ccatcatcct ctacggcgag 1620
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atcaactacg ccgcctgcca cgacaaccac accctctggg acaagaacta cctcgccgcc 1920
aaggccgaca agaagaagga gtggaccgag gaggagctga agaacgccca gaagctcgcc 1980
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tacgagcgca agctccagtt catcgacgtg ttcaactacc acaagggcct catcaagctc 2160
cgcaaggagc acccggcctt ccgcctcaag aacgccgagg agatcaagaa gcacctggag 2220
ttcctcccgg gcgggcgccg catcgtggcc ttcatgctca aggaccacgc cggcggcgac 2280
ccgtggaagg acatcgtggt gatctacaac ggcaacctgg agaagaccac ctacaagctc 2340
ccggagggca agtggaacgt ggtggtgaac tcccagaagg ccggcaccga ggtgatcgag 2400
accgtggagg gcaccatcga gctggacccg ctctccgcct acgtgctcta ccgcgagtcc 2460
gagaaggacg agctgtga 2478

<210> 26
<211> 718
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 26

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ala	Ser
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Ala	Thr	Ser	Met	Glu	Thr	Ile	Lys	Ile	Tyr	Glu	Asn	Lys	Gly	Val	Tyr
			20					25					30		
Lys	Val	Val	Ile	Gly	Glu	Pro	Phe	Pro	Pro	Ile	Glu	Phe	Pro	Leu	Glu
		35					40					45			
Gln	Lys	Ile	Ser	Ser	Asn	Lys	Ser	Leu	Ser	Glu	Leu	Gly	Leu	Thr	Ile
	50					55					60				
Val	Gln	Gln	Gly	Asn	Lys	Val	Ile	Val	Glu	Lys	Ser	Leu	Asp	Leu	Lys
65					70					75					80
Glu	His	Ile	Ile	Gly	Leu	Gly	Glu	Lys	Ala	Phe	Glu	Leu	Asp	Arg	Lys
				85					90					95	
Arg	Lys	Arg	Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys
			100					105					110		
Tyr	Gln	Asp	Pro	Leu	Tyr	Val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys
		115					120					125			
Asp	Gly	Val	Ala	Thr	Gly	Tyr	Phe	Phe	Asn	Ser	Ala	Ser	Lys	Val	Ile
	130					135					140				
Phe	Asp	Val	Gly	Leu	Glu	Glu	Tyr	Asp	Lys	Val	Ile	Val	Thr	Ile	Pro
145					150					155					160
Glu	Asp	Ser	Val	Glu	Phe	Tyr	Val	Ile	Glu	Gly	Pro	Arg	Ile	Glu	Asp
				165					170					175	
Val	Leu	Glu	Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro
			180					185					190		
Met	Trp	Ala	Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln
		195					200					205			
Asp	Lys	Val	Val	Glu	Leu	Val	Asp	Ile	Met	Gln	Lys	Glu	Gly	Phe	Arg
	210					215					220				
Val	Ala	Gly	Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu

225 230 235 240
Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
245 250 255
Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
260 265 270
Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
275 280 285
Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
290 295 300
Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
305 310 315 320
Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
325 330 335
Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
340 345 350
Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
355 360 365
Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
370 375 380
Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
385 390 395 400
Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
405 410 415
Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
420 425 430
Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
435 440 445
Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
450 455 460
Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
465 470 475 480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
485 490 495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
500 505 510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
515 520 525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
530 535 540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
545 550 555 560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
565 570 575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
580 585 590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
595 600 605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
610 615 620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
625 630 635 640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
645 650 655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
660 665 670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
675 680 685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys

690 695 700
Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
705 710 715

<210> 27
<211> 712
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 27
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
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Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
20 25 30
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
35 40 45
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
50 55 60
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
65 70 75 80
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
85 90 95
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
100 105 110
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
115 120 125
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
130 135 140
Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
145 150 155 160
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
165 170 175
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
180 185 190
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
195 200 205
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
210 215 220
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu
225 230 235 240
Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
245 250 255
Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
260 265 270
Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
275 280 285
Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
290 295 300
Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
305 310 315 320
Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
325 330 335
Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
340 345 350

Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
355 360 365
Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
370 375 380
Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
385 390 395 400
Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
405 410 415
Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
420 425 430
Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
435 440 445
Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
450 455 460
Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
465 470 475 480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
485 490 495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
500 505 510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
515 520 525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
530 535 540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
545 550 555 560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
565 570 575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
580 585 590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
595 600 605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
610 615 620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
625 630 635 640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
645 650 655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
660 665 670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
675 680 685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys
690 695 700
Ile Arg Gly Lys Ile Asn Leu Glu
705 710

<210> 28
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 28
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser

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 1               5                  10                  15
Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe
            20                  25                  30
Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro
        35                  40                  45
Asn Glu Val Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
    50                  55                  60
Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
65                  70                  75                  80
Asp Pro Thr Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp
                85                  90                  95
Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
            100                 105                 110
Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
        115                 120                 125
Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
    130                 135                 140
Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
145                 150                 155                 160
Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
                165                 170                 175
Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
            180                 185                 190
Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
        195                 200                 205
Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Leu Glu
    210                 215                 220
Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Glu Tyr Ala Lys
225                 230                 235                 240
Lys Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
                245                 250                 255
Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
            260                 265                 270
Leu Lys Asn His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
        275                 280                 285
Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
    290                 295                 300
Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
305                 310                 315                 320
Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Ile Tyr Asp
                325                 330                 335
Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
            340                 345                 350
Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
        355                 360                 365
Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
    370                 375                 380
Gly Phe Lys Ile Ala Tyr Lys Leu Ala Lys Asp Gly Val Phe Asp Lys
385                 390                 395                 400
Phe Ile Glu Glu Lys Tyr Arg Ser Phe Lys Glu Gly Ile Gly Lys Glu
                405                 410                 415
Ile Val Glu Gly Lys Thr Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
            420                 425                 430
Asp Lys Glu Asp Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
        435                 440                 445
Ser Leu Leu Asn Ser Tyr Ile Val Lys Thr Ile Ala Glu Leu Arg Ser
    450                 455                 460
Glu Lys Asp Glu Leu
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465

<210> 29
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 29
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15
Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
20 25 30
Glu Glu Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
35 40 45
Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
50 55 60
Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
65 70 75 80
Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
85 90 95
Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
100 105 110
Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
115 120 125
Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
130 135 140
Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
145 150 155 160
Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
165 170 175
Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
180 185 190
Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
195 200 205
Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
210 215 220
Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
225 230 235 240
Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
245 250 255
Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
260 265 270
Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
275 280 285
Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
290 295 300
Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
305 310 315 320
Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
325 330 335
Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
340 345 350
Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
355 360 365

Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
370 375 380
Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
385 390 395 400
Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
405 410 415
Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
420 425 430
Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
435 440 445
Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg Ser
450 455 460
Glu Lys Asp Glu Leu
465

<210> 30
<211> 463
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 30
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15
Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
20 25 30
Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
35 40 45
Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
50 55 60
Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
65 70 75 80
Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
85 90 95
Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
100 105 110
Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
115 120 125
Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
130 135 140
Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
145 150 155 160
Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
165 170 175
Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
180 185 190
Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
195 200 205
Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
210 215 220
Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
225 230 235 240
Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
245 250 255
Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe

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                260                 265                 270
Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
            275                 280                 285
Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
        290                 295                 300
Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
305                 310                 315                 320
Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
                325                 330                 335
Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
            340                 345                 350
Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
        355                 360                 365
Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
    370                 375                 380
Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
385                 390                 395                 400
Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
                405                 410                 415
Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
            420                 425                 430
Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
        435                 440                 445
Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
    450                 455                 460


<210> 31
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 31
Met Gly Lys Asn Gly Asn Leu Cys Cys Phe Ser Leu Leu Leu Leu Leu
 1               5                  10                  15
Leu Ala Gly Leu Ala Ser Gly His Gln
            20                  25


<210> 32
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 32
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
 1               5                  10                  15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
            20                  25                  30


<210> 33
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<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 33

Met	Arg	Val	Leu	Leu	Val	Ala	Leu	Ala	Leu	Leu	Ala	Leu	Ala	Ala	Ser
1				5				10						15	
Ala	Thr	Ser	Ala	Lys	Tyr	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Met
			20					25					30		
Gln	Ala	Phe	Tyr	Trp	Asp	Val	Pro	Ser	Gly	Gly	Ile	Trp	Trp	Asp	Thr
		35					40					45			
Ile	Arg	Gln	Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile
	50					55					60				
Trp	Ile	Pro	Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly
65					70					75					80
Tyr	Asp	Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly
				85					90					95	
Thr	Val	Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile
			100					105					110		
Asn	Thr	Ala	His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile
		115					120					125			
Asn	His	Arg	Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp
	130					135					140				
Tyr	Thr	Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala
145					150					155					160
Asn	Tyr	Leu	Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly
				165					170					175	
Thr	Phe	Gly	Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln
			180					185					190		
Tyr	Trp	Leu	Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser
		195					200					205			
Ile	Gly	Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala
	210					215					220				
Trp	Val	Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly
225					230					235					240
Glu	Tyr	Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser
				245					250					255	
Ser	Gly	Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala
			260					265					270		
Ala	Phe	Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn
		275					280					285			
Gly	Gly	Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val
	290					295					300				
Ala	Asn	His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala
305					310					315					320
Phe	Ile	Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr
				325					330					335	
Glu	Glu	Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His
			340					345					350		
Asp	Asn	Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp
		355					360					365			
Glu	Met	Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile
	370					375					380				
Thr	Tyr	Ile	Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val
385					390					395					400

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Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
                405                 410                 415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
            420                 425                 430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
        435                 440                 445
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
    450                 455                 460
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<210> 34
<211> 825
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 34

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1               5                  10                  15
Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
            20                  25                  30
Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
        35                  40                  45
Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
    50                  55                  60
Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
65                  70                  75                  80
Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
                85                  90                  95
Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
            100                 105                 110
Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
        115                 120                 125
Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
    130                 135                 140
Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
145                 150                 155                 160
Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
                165                 170                 175
Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
            180                 185                 190
Asp Asp Tyr Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
        195                 200                 205
Lys Thr Ile Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val
    210                 215                 220
Leu Leu Phe Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn
225                 230                 235                 240
Met Glu Tyr Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp
                245                 250                 255
Leu Asp Gly Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile
            260                 265                 270
Arg Thr Thr Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln
        275                 280                 285
Glu Ser Ala Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu
    290                 295                 300
Asn Asp Arg Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr
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305 310 315 320
Glu Ile His Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys
325 330 335
Asn Lys Gly Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Ala Pro
340 345 350
Gly Gly Val Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr
355 360 365
His Val His Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu
370 375 380
Asp Lys Asp Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu
385 390 395 400
Phe Met Val Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His
405 410 415
Thr Arg Ile Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His
420 425 430
Gly Ile Gly Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile
435 440 445
Gly Glu Leu Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg
450 455 460
Ile Asp Lys Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val
465 470 475 480
Ile Ala Ser Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val
485 490 495
Thr Tyr Trp Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln
500 505 510
Met Gly Leu Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu
515 520 525
His Lys Ile Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly
530 535 540
Trp Gly Ala Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His
545 550 555 560
Val Ala Ala Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val
565 570 575
Phe Asn Pro Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu
580 585 590
Thr Lys Ile Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys
595 600 605
Leu Ile Lys Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala
610 615 620
Ala Cys His Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala
625 630 635 640
Lys Ala Asp Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala
645 650 655
Gln Lys Leu Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe
660 665 670
Leu His Gly Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn
675 680 685
Ser Tyr Asn Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys
690 695 700
Leu Gln Phe Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu
705 710 715 720
Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys
725 730 735
Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met
740 745 750
Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile
755 760 765
Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys

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    770                 775                 780
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
785                 790                 795                 800
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu
                805                 810                 815
Tyr Arg Glu Ser Glu Lys Asp Glu Leu
            820                 825
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<210> 35
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 35

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1               5                  10                  15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
            20                  25                  30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
        35                  40                  45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
    50                  55                  60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65                  70                  75                  80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
                85                  90                  95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
            100                 105                 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
        115                 120                 125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
    130                 135                 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145                 150                 155                 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
                165                 170                 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
            180                 185                 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
        195                 200                 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
    210                 215                 220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225                 230                 235                 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
                245                 250                 255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
            260                 265                 270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
        275                 280                 285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
    290                 295                 300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305                 310                 315                 320
```

Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325 330 335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340 345 350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
355 360 365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
370 375 380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385 390 395 400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
405 410 415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
420 425 430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
435 440 445
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
450 455 460

<210> 36
<211> 718
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 36
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15
Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
20 25 30
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
35 40 45
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
50 55 60
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
65 70 75 80
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
85 90 95
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
100 105 110
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
115 120 125
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
130 135 140
Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
145 150 155 160
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
165 170 175
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
180 185 190
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
195 200 205
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
210 215 220
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu

225 230 235 240
Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
245 250 255
Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
260 265 270
Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
275 280 285
Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
290 295 300
Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
305 310 315 320
Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
325 330 335
Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
340 345 350
Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
355 360 365
Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
370 375 380
Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
385 390 395 400
Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
405 410 415
Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
420 425 430
Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
435 440 445
Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
450 455 460
Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
465 470 475 480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
485 490 495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
500 505 510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
515 520 525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
530 535 540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
545 550 555 560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
565 570 575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
580 585 590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
595 600 605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
610 615 620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
625 630 635 640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
645 650 655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
660 665 670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
675 680 685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys

690 695 700
Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
705 710 715

<210> 37
<211> 1434
<212> DNA
<213> Thermotoga maritima

<400> 37
atgaaagaaa ccgctgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
accctggtgc cacgcggttc catggccgag ttcttcccgg agatcccgaa gatccagttc 120
gagggcaagg agtccaccaa cccgctcgcc ttccgcttct acgacccgaa cgaggtgatc 180
gacggcaagc cgctcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
aacgagggcc gcgacccgtt cggcgacccg accgccgagc gcccgtggaa ccgcttctcc 300
gacccgatgg acaaggcctt cgcccgcgtg gacgccctct tcgagttctg cgagaagctc 360
aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggagggcaa gaccctccgc 420
gagaccaaca agatcctcga caaggtggtg gagcgcatca aggagcgcat gaaggactcc 480
aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgcta catgcacggc 540
gccgccacca cctgctccgc cgacgtgttc gcctacgccg ccgcccaggt gaagaaggcc 600
ctggagatca ccaaggagct gggcggcgag ggctacgtgt tctggggcgg ccgcgagggc 660
tacgagaccc tcctcaacac cgacctcggc ctggagctgg agaacctcgc ccgcttcctc 720
cgcatggccg tggagtacgc caagaagatc ggcttcaccg gccagttcct catcgagccg 780
aagccgaagg agccgaccaa gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
ctcaagaacc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
ctcgccggcc acaccttcca gcacgagctg cgcatggccc gcatcctcgg caagctcggc 960
tccatcgacg ccaaccaggg cgacctcctc ctcggctggg acaccgacca gttcccgacc 1020
aacatctacg acaccaccct cgccatgtac gaggtgatca aggccggcgg cttcaccaag 1080
ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct acaaggtgga ggacctcttc 1140
atcggccaca tcgccggcat ggacaccttc gccctcggct tcaagatcgc ctacaagctc 1200
gccaaggacg gcgtgttcga caagttcatc gaggagaagt accgctcctt caaggagggc 1260
atcggcaagg agatcgtgga gggcaagacc gacttcgaga agctggagga gtacatcatc 1320
gacaaggagg acatcgagct gccgtccggc aagcaggagt acctggagtc cctcctcaac 1380
tcctacatcg tgaagaccat cgccgagctg cgctccgaga aggacgagct gtga 1434

<210> 38
<211> 477
<212> PRT
<213> Thermotoga maritima

<400> 38
Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
1 5 10 15
Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
20 25 30
Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
35 40 45
Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val Ile Asp Gly Lys Pro
50 55 60
Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
65 70 75 80
Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Glu Arg Pro Trp
85 90 95
Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
100 105 110
Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
115 120 125

Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
130 135 140
Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
145 150 155 160
Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
165 170 175
Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
180 185 190
Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
195 200 205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
210 215 220
Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn Leu Ala Arg Phe Leu
225 230 235 240
Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly Phe Thr Gly Gln Phe
245 250 255
Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
260 265 270
Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn His Gly Leu Asp Glu
275 280 285
Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
290 295 300
Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
305 310 315 320
Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
325 330 335
Gln Phe Pro Thr Asn Ile Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
340 345 350
Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
355 360 365
Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
370 375 380
Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Ile Ala Tyr Lys Leu
385 390 395 400
Ala Lys Asp Gly Val Phe Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
405 410 415
Phe Lys Glu Gly Ile Gly Lys Glu Ile Val Glu Gly Lys Thr Asp Phe
420 425 430
Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Asp Ile Glu Leu Pro
435 440 445
Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Leu Asn Ser Tyr Ile Val
450 455 460
Lys Thr Ile Ala Glu Leu Arg Ser Glu Lys Asp Glu Leu
465 470 475

<210> 39
<211> 1434
<212> DNA
<213> Thermotoga neapolitana

<400> 39
atgaaagaaa ccgctgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
accctggtgc cacgcggttc catggccgag ttcttcccgg agatcccgaa ggtgcagttc 120
gagggcaagg agtccaccaa cccgctcgcc ttcaagttct acgacccgga ggagatcatc 180
gacggcaagc cgctcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
aacgagggcc gcgacccgtt cggcgacccg accgccgacc gcccgtggaa ccgctacacc 300
gacccgatgg acaaggcctt cgcccgcgtg gacgccctct tcgagttctg cgagaagctc 360

aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggagggcaa gaccctccgc 420
gagaccaaca agatcctcga caaggtggtg gagcgcatca aggagcgcat gaaggactcc 480
aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgcta catgcacggc 540
gccgccacca cctgctccgc cgacgtgttc gcctacgccg ccgcccaggt gaagaaggcc 600
ctggagatca ccaaggagct gggcggcgag ggctacgtgt tctggggcgg ccgcgagggc 660
tacgagaccc tcctcaacac cgacctcggc ttcgagctgg agaacctcgc ccgcttcctc 720
cgcatggccg tggactacgc caagcgcatc ggcttcaccg gccagttcct catcgagccg 780
aagccgaagg agccgaccaa gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
ctcaagtccc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
ctcgccggcc acaccttcca gcacgagctg cgcatggccc gcatcctcgg caagctcggc 960
tccatcgacg ccaaccaggg cgacctcctc ctcggctggg acaccgacca gttcccgacc 1020
aacgtgtacg acaccaccct cgccatgtac gaggtgatca aggccggcgg cttcaccaag 1080
ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct acaaggtgga ggacctcttc 1140
atcggccaca tcgccggcat ggacaccttc gccctcggct tcaaggtggc ctacaagctc 1200
gtgaaggacg gcgtgctcga caagttcatc gaggagaagt accgctcctt ccgcgagggc 1260
atcggccgcg acatcgtgga gggcaaggtg gacttcgaga agctggagga gtacatcatc 1320
gacaaggaga ccatcgagct gccgtccggc aagcaggagt acctggagtc cctcatcaac 1380
tcctacatcg tgaagaccat cctggagctg cgctccgaga aggacgagct gtga 1434

<210> 40
<211> 477
<212> PRT
<213> Thermotoga neapolitana

<400> 40

Met	Lys	Glu	Thr	Ala	Ala	Ala	Lys	Phe	Glu	Arg	Gln	His	Met	Asp	Ser
1				5					10					15	
Pro	Asp	Leu	Gly	Thr	Leu	Val	Pro	Arg	Gly	Ser	Met	Ala	Glu	Phe	Phe
			20					25					30		
Pro	Glu	Ile	Pro	Lys	Val	Gln	Phe	Glu	Gly	Lys	Glu	Ser	Thr	Asn	Pro
		35					40					45			
Leu	Ala	Phe	Lys	Phe	Tyr	Asp	Pro	Glu	Glu	Ile	Ile	Asp	Gly	Lys	Pro
	50					55					60				
Leu	Lys	Asp	His	Leu	Lys	Phe	Ser	Val	Ala	Phe	Trp	His	Thr	Phe	Val
65					70					75					80
Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly	Asp	Pro	Thr	Ala	Asp	Arg	Pro	Trp
				85					90					95	
Asn	Arg	Tyr	Thr	Asp	Pro	Met	Asp	Lys	Ala	Phe	Ala	Arg	Val	Asp	Ala
			100					105					110		
Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu	Asn	Ile	Glu	Tyr	Phe	Cys	Phe	His
		115					120					125			
Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly	Lys	Thr	Leu	Arg	Glu	Thr	Asn	Lys
	130					135					140				
Ile	Leu	Asp	Lys	Val	Val	Glu	Arg	Ile	Lys	Glu	Arg	Met	Lys	Asp	Ser
145					150					155					160
Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr	Ala	Asn	Leu	Phe	Ser	His	Pro	Arg
				165					170					175	
Tyr	Met	His	Gly	Ala	Ala	Thr	Thr	Cys	Ser	Ala	Asp	Val	Phe	Ala	Tyr
			180					185					190		
Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala	Leu	Glu	Ile	Thr	Lys	Glu	Leu	Gly
		195					200					205			
Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly	Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu
	210					215					220				
Leu	Asn	Thr	Asp	Leu	Gly	Phe	Glu	Leu	Glu	Asn	Leu	Ala	Arg	Phe	Leu
225					230					235					240
Arg	Met	Ala	Val	Asp	Tyr	Ala	Lys	Arg	Ile	Gly	Phe	Thr	Gly	Gln	Phe
				245					250					255	
Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu	Pro	Thr	Lys	His	Gln	Tyr	Asp	Phe

260 265 270
Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser His Gly Leu Asp Glu
275 280 285
Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
290 295 300
Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
305 310 315 320
Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
325 330 335
Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
340 345 350
Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
355 360 365
Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
370 375 380
Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Val Ala Tyr Lys Leu
385 390 395 400
Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
405 410 415
Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu Gly Lys Val Asp Phe
420 425 430
Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Thr Ile Glu Leu Pro
435 440 445
Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile Asn Ser Tyr Ile Val
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Lys Thr Ile Leu Glu Leu Arg Ser Glu Lys Asp Glu Leu
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<210> 41
<211> 1435
<212> DNA
<213> Thermotoga maritima

<400> 41
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gagatcccga agatccagtt cgagggcaag gagtccacca acccgctcgc cttccgcttc 180
tacgacccga acgaggtgat cgacggcaag ccgctcaagg accacctcaa gttctccgtg 240
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cgcccgtgga accgcttctc cgacccgatg gacaaggcct tcgcccgcgt ggacgccctc 360
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cggagggcaa gaccctccgc gagaccaaca agatcctcga caaggtggtg gagcgcatca 480
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ccgcccaggt gaagaaggcc ctggagatca ccaaggagct gggcggcgag ggctacgtgt 660
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gccagttcct catcgagccg aagccgaagg agccgaccaa gcaccagtac gcttcgacgt 840
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cgaggccaac cacgccaccc tcgccggcca caccttccag cacgagctgc gcatggcccg 960
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caccgaccag ttcccgacca acatctacga caccaccctc gccatgtacg aggtgatcaa 1080
ggccggcggc ttcaccaagg gcggcctcaa cttcgacgcc aaggtgcgcc gcgcctccta 1140
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caagatcgcc tacaagctcg ccaaggacgg cgtgttcgac aagttcatcg aggagaagta 1260
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gctggaggag tacatcatcg acaaggagga catcgagctg ccgtccggca agcaggagta 1380

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<210> 42
<211> 478
<212> PRT
<213> Thermotoga maritima

<400> 42

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Ile	Pro	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Ile	Gln	Phe	Glu
		35					40					45			
Gly	Lys	Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Arg	Phe	Tyr	Asp	Pro	Asn
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Glu	Val	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser	Val
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Ala	Phe	Trp	His	Thr	Phe	Val	Asn	Glu	Gly	Arg	Asp	Pro	Phe	Gly	Asp
				85					90					95	
Pro	Thr	Ala	Glu	Arg	Pro	Trp	Asn	Arg	Phe	Ser	Asp	Pro	Met	Asp	Lys
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Ala	Phe	Ala	Arg	Val	Asp	Ala	Leu	Phe	Glu	Phe	Cys	Glu	Lys	Leu	Asn
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Ile	Glu	Tyr	Phe	Cys	Phe	His	Asp	Arg	Asp	Ile	Ala	Pro	Glu	Gly	Lys
	130					135					140				
Thr	Leu	Arg	Glu	Thr	Asn	Lys	Ile	Leu	Asp	Lys	Val	Val	Glu	Arg	Ile
145					150					155					160
Lys	Glu	Arg	Met	Lys	Asp	Ser	Asn	Val	Lys	Leu	Leu	Trp	Gly	Thr	Ala
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Asn	Leu	Phe	Ser	His	Pro	Arg	Tyr	Met	His	Gly	Ala	Ala	Thr	Thr	Cys
			180					185					190		
Ser	Ala	Asp	Val	Phe	Ala	Tyr	Ala	Ala	Ala	Gln	Val	Lys	Lys	Ala	Leu
		195					200					205			
Glu	Ile	Thr	Lys	Glu	Leu	Gly	Gly	Glu	Gly	Tyr	Val	Phe	Trp	Gly	Gly
	210					215					220				
Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asp	Leu	Gly	Leu	Glu	Leu
225					230					235					240
Glu	Asn	Leu	Ala	Arg	Phe	Leu	Arg	Met	Ala	Val	Glu	Tyr	Ala	Lys	Lys
				245					250					255	
Ile	Gly	Phe	Thr	Gly	Gln	Phe	Leu	Ile	Glu	Pro	Lys	Pro	Lys	Glu	Pro
			260					265					270		
Thr	Lys	His	Gln	Tyr	Asp	Phe	Asp	Val	Ala	Thr	Ala	Tyr	Ala	Phe	Leu
		275					280					285			
Lys	Asn	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala	Asn
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His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met	Ala
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Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp	Leu
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Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Ile	Tyr	Asp	Thr
			340					345					350		
Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys	Gly
		355					360					365			
Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val	Glu
	370					375					380				
Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu	Gly
385					390					395					400

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Phe Lys Ile Ala Tyr Lys Leu Ala Lys Asp Gly Val Phe Asp Lys Phe
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Ile Glu Glu Lys Tyr Arg Ser Phe Lys Glu Gly Ile Gly Lys Glu Ile
            420                 425                 430
Val Glu Gly Lys Thr Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp
        435                 440                 445
Lys Glu Asp Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser
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Leu Leu Asn Ser Tyr Ile Val Lys Thr Ile Ala Glu Leu Arg
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<210> 43
<211> 1436
<212> DNA
<213> Thermotoga neapolitana

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gagatcccga aggtgcagtt cgagggcaag gagtccacca acccgctcgc cttcaagttc 180
tacgacccgg aggagatcat cgacggcaag ccgctcaagg accacctcaa gttctccgtg 240
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cggagggcaa gaccctccgc gagaccaaca agatcctcga caaggtggtg gagcgcatca 480
aggagcgcat gaaggactcc aacgtgaagc tcctctgggg caccgccaac ctcttctccc 540
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ccgcccaggt gaagaaggcc ctggagatca ccaaggagct gggcggcgag ggctacgtgt 660
tctggggcgg ccgcgagggc tacgagaccc tcctcaacac cgacctcggc ttcgagctgg 720
agaacctcgc ccgcttcctc cgcatggccg tggactacgc caagcgcatc ggcttcaccg 780
gccagttcct catcgagccg aagccgaagg agccgaccaa gcaccagtac gacttcgacg 840
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<210> 44
<211> 478
<212> PRT
<213> Thermotoga neapolitana

<400> 44
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            20                  25                  30
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        35                  40                  45
Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu
    50                  55                  60
Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val
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65 70 75 80
Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
85 90 95
Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys
100 105 110
Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
115 120 125
Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
130 135 140
Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile
145 150 155 160
Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala
165 170 175
Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys
180 185 190
Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu
195 200 205
Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly
210 215 220
Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu
225 230 235 240
Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg
245 250 255
Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro
260 265 270
Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu
275 280 285
Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn
290 295 300
His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala
305 310 315 320
Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu
325 330 335
Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr
340 345 350
Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly
355 360 365
Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu
370 375 380
Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly
385 390 395 400
Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe
405 410 415
Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile
420 425 430
Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp
435 440 445
Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser
450 455 460
Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
465 470 475

<210> 45
<211> 1095
<212> PRT
<213> Aspergillus shirousami

<400> 45

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			20					25					30		
Ala	Asp	Gln	Lys	Tyr	Cys	Gly	Gly	Thr	Trp	Gln	Gly	Ile	Ile	Asp	Lys
		35					40					45			
Leu	Asp	Tyr	Ile	Gln	Gly	Met	Gly	Phe	Thr	Ala	Ile	Trp	Ile	Thr	Pro
	50					55					60				
Val	Thr	Ala	Gln	Leu	Pro	Gln	Thr	Thr	Ala	Tyr	Gly	Asp	Ala	Tyr	His
65					70					75					80
Gly	Tyr	Trp	Gln	Gln	Asp	Ile	Tyr	Ser	Leu	Asn	Glu	Asn	Tyr	Gly	Thr
				85					90					95	
Ala	Asp	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Ala	Leu	His	Glu	Arg	Gly	Met
			100					105					110		
Tyr	Leu	Met	Val	Asp	Val	Val	Ala	Asn	His	Met	Gly	Tyr	Asp	Gly	Ala
		115					120					125			
Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys	Pro	Phe	Ser	Ser	Gln	Asp
	130					135					140				
Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn	Tyr	Glu	Asp	Gln	Thr	Gln
145					150					155					160
Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr	Val	Ser	Leu	Pro	Asp	Leu
				165					170					175	
Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu	Trp	Tyr	Asp	Trp	Val	Gly
			180					185					190		
Ser	Leu	Val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly	Leu	Arg	Ile	Asp	Thr	Val
		195					200					205			
Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly	Tyr	Asn	Lys	Ala	Ala	Gly
	210					215					220				
Val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Val	Asp	Pro	Ala	Tyr	Thr	Cys
225					230					235					240
Pro	Tyr	Gln	Asn	Val	Met	Asp	Gly	Val	Leu	Asn	Tyr	Pro	Ile	Tyr	Tyr
				245					250					255	
Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser	Met	Asp	Asp	Leu
			260					265					270		
Tyr	Asn	Met	Ile	Asn	Thr	Val	Lys	Ser	Asp	Cys	Pro	Asp	Ser	Thr	Leu
		275					280					285			
Leu	Gly	Thr	Phe	Val	Glu	Asn	His	Asp	Asn	Pro	Arg	Phe	Ala	Ser	Tyr
	290					295					300				
Thr	Asn	Asp	Ile	Ala	Leu	Ala	Lys	Asn	Val	Ala	Ala	Phe	Ile	Ile	Leu
305					310					315					320
Asn	Asp	Gly	Ile	Pro	Ile	Ile	Tyr	Ala	Gly	Gln	Glu	Gln	His	Tyr	Ala
				325					330					335	
Gly	Gly	Asn	Asp	Pro	Ala	Asn	Arg	Glu	Ala	Thr	Trp	Leu	Ser	Gly	Tyr
			340					345					350		
Pro	Thr	Asp	Ser	Glu	Leu	Tyr	Lys	Leu	Ile	Ala	Ser	Ala	Asn	Ala	Ile
		355					360					365			
Arg	Asn	Tyr	Ala	Ile	Ser	Lys	Asp	Thr	Gly	Phe	Val	Thr	Tyr	Lys	Asn
	370					375					380				
Trp	Pro	Ile	Tyr	Lys	Asp	Asp	Thr	Thr	Ile	Ala	Met	Arg	Lys	Gly	Thr
385					390					395					400
Asp	Gly	Ser	Gln	Ile	Val	Thr	Ile	Leu	Ser	Asn	Lys	Gly	Ala	Ser	Gly
				405					410					415	
Asp	Ser	Tyr	Thr	Leu	Ser	Leu	Ser	Gly	Ala	Gly	Tyr	Thr	Ala	Gly	Gln
			420					425					430		
Gln	Leu	Thr	Glu	Val	Ile	Gly	Cys	Thr	Thr	Val	Thr	Val	Gly	Ser	Asp
		435					440					445			
Gly	Asn	Val	Pro	Val	Pro	Met	Ala	Gly	Gly	Leu	Pro	Arg	Val	Leu	Tyr

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Ala Thr Leu Asp Ser Trp Leu Ser Asn Glu Ala Thr Val Ala Arg Thr
                485                 490                 495
Ala Ile Leu Asn Asn Ile Gly Ala Asp Gly Ala Trp Val Ser Gly Ala
            500                 505                 510
Asp Ser Gly Ile Val Val Ala Ser Pro Ser Thr Asp Asn Pro Asp Tyr
        515                 520                 525
Phe Tyr Thr Trp Thr Arg Asp Ser Gly Ile Val Leu Lys Thr Leu Val
    530                 535                 540
Asp Leu Phe Arg Asn Gly Asp Thr Asp Leu Leu Ser Thr Ile Glu His
545                 550                 555                 560
Tyr Ile Ser Ser Gln Ala Ile Ile Gln Gly Val Ser Asn Pro Ser Gly
                565                 570                 575
Asp Leu Ser Ser Gly Gly Leu Gly Glu Pro Lys Phe Asn Val Asp Glu
            580                 585                 590
Thr Ala Tyr Ala Gly Ser Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala
        595                 600                 605
Leu Arg Ala Thr Ala Met Ile Gly Phe Gly Gln Trp Leu Leu Asp Asn
    610                 615                 620
Gly Tyr Thr Ser Ala Ala Thr Glu Ile Val Trp Pro Leu Val Arg Asn
625                 630                 635                 640
Asp Leu Ser Tyr Val Ala Gln Tyr Trp Asn Gln Thr Gly Tyr Asp Leu
                645                 650                 655
Trp Glu Glu Val Asn Gly Ser Ser Phe Phe Thr Ile Ala Val Gln His
            660                 665                 670
Arg Ala Leu Val Glu Gly Ser Ala Phe Ala Thr Ala Val Gly Ser Ser
        675                 680                 685
Cys Ser Trp Cys Asp Ser Gln Ala Pro Gln Ile Leu Cys Tyr Leu Gln
    690                 695                 700
Ser Phe Trp Thr Gly Ser Tyr Ile Leu Ala Asn Phe Asp Ser Ser Arg
705                 710                 715                 720
Ser Gly Lys Asp Thr Asn Thr Leu Leu Gly Ser Ile His Thr Phe Asp
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Pro Glu Ala Gly Cys Asp Asp Ser Thr Phe Gln Pro Cys Ser Pro Arg
            740                 745                 750
Ala Leu Ala Asn His Lys Glu Val Val Asp Ser Phe Arg Ser Ile Tyr
        755                 760                 765
Thr Leu Asn Asp Gly Leu Ser Asp Ser Glu Ala Val Ala Val Gly Arg
    770                 775                 780
Tyr Pro Glu Asp Ser Tyr Tyr Asn Gly Asn Pro Trp Phe Leu Cys Thr
785                 790                 795                 800
Leu Ala Ala Ala Glu Gln Leu Tyr Asp Ala Leu Tyr Gln Trp Asp Lys
                805                 810                 815
Gln Gly Ser Leu Glu Ile Thr Asp Val Ser Leu Asp Phe Phe Lys Ala
            820                 825                 830
Leu Tyr Ser Gly Ala Ala Thr Gly Thr Tyr Ser Ser Ser Ser Ser Thr
        835                 840                 845
Tyr Ser Ser Ile Val Ser Ala Val Lys Thr Phe Ala Asp Gly Phe Val
    850                 855                 860
Ser Ile Val Glu Thr His Ala Ala Ser Asn Gly Ser Leu Ser Glu Gln
865                 870                 875                 880
Phe Asp Lys Ser Asp Gly Asp Glu Leu Ser Ala Arg Asp Leu Thr Trp
                885                 890                 895
Ser Tyr Ala Ala Leu Leu Thr Ala Asn Asn Arg Arg Asn Ser Val Val
            900                 905                 910
Pro Pro Ser Trp Gly Glu Thr Ser Ala Ser Ser Val Pro Gly Thr Cys
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        915                 920                 925
Ala Ala Thr Ser Ala Ser Gly Thr Tyr Ser Ser Val Thr Val Thr Ser
    930                 935                 940
Trp Pro Ser Ile Val Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Thr
945                 950                 955                 960
Thr Gly Ser Gly Gly Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala
                965                 970                 975
Ser Lys Thr Ser Thr Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr
            980                 985                 990
Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr Thr Thr Tyr Gly Glu
        995                 1000                1005
Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Glu Thr
    1010                1015                1020
Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr Ser Ser Asn Pro
1025                1030                1035                1040
Pro Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr
                1045                1050                1055
Lys Phe Ile Arg Val Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp
            1060                1065                1070
Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly Glu Ser Thr Ala
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Thr Val Thr Asp Thr Trp Arg
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<210> 46
<211> 3285
<212> DNA
<213> Aspergillus shirousami

<400> 46

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<210> 47
<211> 679
<212> PRT
<213> Thermoanaerobacterium thermosaccharolyticum

<400> 47

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Phe	Asn	Asn	Ile	Ser	Ala	Val	Asn	Gly	Pro	Gly	Glu	Glu	Asp	Thr	Trp
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Ala	Ser	Ala	Gln	Lys	Gln	Gly	Val	Gly	Thr	Ala	Asn	Asn	Tyr	Val	Ser
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Arg	Val	Trp	Phe	Thr	Leu	Ala	Asn	Gly	Ala	Ile	Ser	Glu	Val	Tyr	Tyr
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Pro	Thr	Ile	Asp	Thr	Ala	Asp	Val	Lys	Glu	Ile	Lys	Phe	Ile	Val	Thr
65					70					75					80
Asp	Gly	Lys	Ser	Phe	Val	Ser	Asp	Glu	Thr	Lys	Asp	Ala	Ile	Ser	Lys
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Val	Glu	Lys	Phe	Thr	Asp	Lys	Ser	Leu	Gly	Tyr	Lys	Leu	Val	Asn	Thr
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Asp	Lys	Lys	Gly	Arg	Tyr	Arg	Ile	Thr	Lys	Glu	Ile	Phe	Thr	Asp	Val
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Lys	Arg	Asn	Ser	Leu	Ile	Met	Lys	Ala	Lys	Phe	Glu	Ala	Leu	Glu	Gly
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Ser	Ile	His	Asp	Tyr	Lys	Leu	Tyr	Leu	Ala	Tyr	Asp	Pro	His	Ile	Lys
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Asn	Gln	Gly	Ser	Tyr	Asn	Glu	Gly	Tyr	Val	Ile	Lys	Ala	Asn	Asn	Asn
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Glu	Met	Leu	Met	Ala	Lys	Arg	Asp	Asn	Val	Tyr	Thr	Ala	Leu	Ser	Ser

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Ser Ala Arg Gly Asn Ile Ile Glu Gly Ala Glu Ile Asp Leu Thr Lys
225                 230                 235                 240
Asn Ser Glu Phe Glu Ile Val Leu Ser Phe Gly Gly Ser Asp Ser Glu
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Ala Ala Lys Thr Ala Leu Glu Thr Leu Gly Glu Asp Tyr Asn Asn Leu
            260                 265                 270
Lys Asn Asn Tyr Ile Asp Glu Trp Thr Lys Tyr Cys Asn Thr Leu Asn
        275                 280                 285
Asn Phe Asn Gly Lys Ala Asn Ser Leu Tyr Tyr Asn Ser Met Met Ile
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Leu Lys Ala Ser Glu Asp Lys Thr Asn Lys Gly Ala Tyr Ile Ala Ser
305                 310                 315                 320
Leu Ser Ile Pro Trp Gly Asp Gly Gln Arg Asp Asp Asn Thr Gly Gly
                325                 330                 335
Tyr His Leu Val Trp Ser Arg Asp Leu Tyr His Val Ala Asn Ala Phe
            340                 345                 350
Ile Ala Ala Gly Asp Val Asp Ser Ala Asn Arg Ser Leu Asp Tyr Leu
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Ala Lys Val Val Lys Asp Asn Gly Met Ile Pro Gln Asn Thr Trp Ile
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Ser Gly Lys Pro Tyr Trp Thr Ser Ile Gln Leu Asp Glu Gln Ala Asp
385                 390                 395                 400
Pro Ile Ile Leu Ser Tyr Arg Leu Lys Arg Tyr Asp Leu Tyr Asp Ser
                405                 410                 415
Leu Val Lys Pro Leu Ala Asp Phe Ile Ile Lys Ile Gly Pro Lys Thr
            420                 425                 430
Gly Gln Glu Arg Trp Glu Glu Ile Gly Gly Tyr Ser Pro Ala Thr Met
        435                 440                 445
Ala Ala Glu Val Ala Gly Leu Thr Cys Ala Ala Tyr Ile Ala Glu Gln
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Asn Lys Asp Tyr Glu Ser Ala Gln Lys Tyr Gln Glu Lys Ala Asp Asn
465                 470                 475                 480
Trp Gln Lys Leu Ile Asp Asn Leu Thr Tyr Thr Glu Asn Gly Pro Leu
                485                 490                 495
Gly Asn Gly Gln Tyr Tyr Ile Arg Ile Ala Gly Leu Ser Asp Pro Asn
            500                 505                 510
Ala Asp Phe Met Ile Asn Ile Ala Asn Gly Gly Gly Val Tyr Asp Gln
        515                 520                 525
Lys Glu Ile Val Asp Pro Ser Phe Leu Glu Leu Val Arg Leu Gly Val
    530                 535                 540
Lys Ser Ala Asp Asp Pro Lys Ile Leu Asn Thr Leu Lys Val Val Asp
545                 550                 555                 560
Ser Thr Ile Lys Val Asp Thr Pro Lys Gly Pro Ser Trp Tyr Arg Tyr
                565                 570                 575
Asn His Asp Gly Tyr Gly Glu Pro Ser Lys Thr Glu Leu Tyr His Gly
            580                 585                 590
Ala Gly Lys Gly Arg Leu Trp Pro Leu Leu Thr Gly Glu Arg Gly Met
        595                 600                 605
Tyr Glu Ile Ala Ala Gly Lys Asp Ala Thr Pro Tyr Val Lys Ala Met
    610                 615                 620
Glu Lys Phe Ala Asn Glu Gly Gly Ile Ile Ser Glu Gln Val Trp Glu
625                 630                 635                 640
Asp Thr Gly Leu Pro Thr Asp Ser Ala Ser Pro Leu Asn Trp Ala His
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Asp Met Pro Asp Ile Val Tyr
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<210> 48
<211> 2037
<212> DNA
<213> Thermoanaerobacterium thermosaccharolyticum

<220>
<223> synthetic

<400> 48
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gacggcaagt ccttcgtgtc cgacgagacc aaggacgcca tctccaaggt ggagaagttc 300
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<210> 49
<211> 579
<212> PRT
<213> Rhizopus oryzae

<400> 49
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Ser Lys Lys Val Thr Val Ile Tyr Ala Asp Gly Ser Asp Asn Trp Asn
        35                  40                  45
Asn Asn Gly Asn Thr Ile Ala Ala Ser Tyr Ser Ala Pro Ile Ser Gly
    50                  55                  60
Ser Asn Tyr Glu Tyr Trp Thr Phe Ser Ala Ser Ile Asn Gly Ile Lys
65                  70                  75                  80
Glu Phe Tyr Ile Lys Tyr Glu Val Ser Gly Lys Thr Tyr Tyr Asp Asn
                85                  90                  95
Asn Asn Ser Ala Asn Tyr Gln Val Ser Thr Ser Lys Pro Thr Thr Thr
            100                 105                 110
Thr Ala Thr Ala Thr Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Thr
        115                 120                 125
Pro Pro Ser Arg Ser Glu Pro Ala Thr Phe Pro Thr Gly Asn Ser Thr
    130                 135                 140
Ile Ser Ser Trp Ile Lys Lys Gln Glu Gly Ile Ser Arg Phe Ala Met
145                 150                 155                 160
Leu Arg Asn Ile Asn Pro Pro Gly Ser Ala Thr Gly Phe Ile Ala Ala
                165                 170                 175
Ser Leu Ser Thr Ala Gly Pro Asp Tyr Tyr Tyr Ala Trp Thr Arg Asp
            180                 185                 190
Ala Ala Leu Thr Ser Asn Val Ile Val Tyr Glu Tyr Asn Thr Thr Leu
        195                 200                 205
Ser Gly Asn Lys Thr Ile Leu Asn Val Leu Lys Asp Tyr Val Thr Phe
    210                 215                 220
Ser Val Lys Thr Gln Ser Thr Ser Thr Val Cys Asn Cys Leu Gly Glu
225                 230                 235                 240
Pro Lys Phe Asn Pro Asp Ala Ser Gly Tyr Thr Gly Ala Trp Gly Arg
                245                 250                 255
Pro Gln Asn Asp Gly Pro Ala Glu Arg Ala Thr Thr Phe Ile Leu Phe
            260                 265                 270
Ala Asp Ser Tyr Leu Thr Gln Thr Lys Asp Ala Ser Tyr Val Thr Gly
        275                 280                 285
Thr Leu Lys Pro Ala Ile Phe Lys Asp Leu Asp Tyr Val Val Asn Val
    290                 295                 300
Trp Ser Asn Gly Cys Phe Asp Leu Trp Glu Glu Val Asn Gly Val His
305                 310                 315                 320
Phe Tyr Thr Leu Met Val Met Arg Lys Gly Leu Leu Leu Gly Ala Asp
                325                 330                 335
Phe Ala Lys Arg Asn Gly Asp Ser Thr Arg Ala Ser Thr Tyr Ser Ser
            340                 345                 350
Thr Ala Ser Thr Ile Ala Asn Lys Ile Ser Ser Phe Trp Val Ser Ser
        355                 360                 365
Asn Asn Trp Ile Gln Val Ser Gln Ser Val Thr Gly Gly Val Ser Lys
    370                 375                 380
Lys Gly Leu Asp Val Ser Thr Leu Leu Ala Ala Asn Leu Gly Ser Val
385                 390                 395                 400
Asp Asp Gly Phe Phe Thr Pro Gly Ser Glu Lys Ile Leu Ala Thr Ala
                405                 410                 415
Val Ala Val Glu Asp Ser Phe Ala Ser Leu Tyr Pro Ile Asn Lys Asn
            420                 425                 430
Leu Pro Ser Tyr Leu Gly Asn Ser Ile Gly Arg Tyr Pro Glu Asp Thr
        435                 440                 445
Tyr Asn Gly Asn Gly Asn Ser Gln Gly Asn Ser Trp Phe Leu Ala Val
    450                 455                 460
Thr Gly Tyr Ala Glu Leu Tyr Tyr Arg Ala Ile Lys Glu Trp Ile Gly
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465 470 475 480
Asn Gly Gly Val Thr Val Ser Ser Ile Ser Leu Pro Phe Phe Lys Lys
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Phe Asp Ser Ser Ala Thr Ser Gly Lys Lys Tyr Thr Val Gly Thr Ser
500 505 510
Asp Phe Asn Asn Leu Ala Gln Asn Ile Ala Leu Ala Ala Asp Arg Phe
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Leu Ser Thr Val Gln Leu His Ala His Asn Asn Gly Ser Leu Ala Glu
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Glu Phe Asp Arg Thr Thr Gly Leu Ser Thr Gly Ala Arg Asp Leu Thr
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Trp Ser His Ala Ser Leu Ile Thr Ala Ser Tyr Ala Lys Ala Gly Ala
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<210> 50
<211> 1737
<212> DNA
<213> Rhizopus oryzae

<400> 50
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<210> 51
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 51

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			20					25					30		
Gln	Gly	Phe	Asn	Trp	Glu	Ser	Trp	Lys	Lys	Gln	Gly	Gly	Trp	Tyr	Asn
		35					40					45			
Tyr	Leu	Leu	Gly	Arg	Val	Asp	Asp	Ile	Ala	Ala	Thr	Gly	Ala	Thr	His
	50					55					60				
Val	Trp	Leu	Pro	Gln	Pro	Ser	His	Ser	Val	Ala	Pro	Gln	Gly	Tyr	Met
65					70					75					80
Pro	Gly	Arg	Leu	Tyr	Asp	Leu	Asp	Ala	Ser	Lys	Tyr	Gly	Thr	His	Ala
				85					90					95	
Glu	Leu	Lys	Ser	Leu	Thr	Ala	Ala	Phe	His	Ala	Lys	Gly	Val	Gln	Cys
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Val	Ala	Asp	Val	Val	Ile	Asn	His	Arg	Cys	Ala	Asp	Tyr	Lys	Asp	Gly
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Arg	Gly	Ile	Tyr	Cys	Val	Phe	Glu	Gly	Gly	Thr	Pro	Asp	Ser	Arg	Leu
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Asp	Trp	Gly	Pro	Asp	Met	Ile	Cys	Ser	Asp	Asp	Thr	Gln	Tyr	Ser	Asn
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Gly	Arg	Gly	His	Arg	Asp	Thr	Gly	Ala	Asp	Phe	Ala	Ala	Ala	Pro	Asp
				165					170					175	
Ile	Asp	His	Leu	Asn	Pro	Arg	Val	Gln	Gln	Glu	Leu	Ser	Asp	Trp	Leu
			180					185					190		
Asn	Trp	Leu	Lys	Ser	Asp	Leu	Gly	Phe	Asp	Gly	Trp	Arg	Leu	Asp	Phe
		195					200					205			
Ala	Lys	Gly	Tyr	Ser	Ala	Ala	Val	Ala	Lys	Val	Tyr	Val	Asp	Ser	Thr
	210					215					220				
Ala	Pro	Thr	Phe	Val	Val	Ala	Glu	Ile	Trp	Ser	Ser	Leu	His	Tyr	Asp
225					230					235					240
Gly	Asn	Gly	Glu	Pro	Ser	Ser	Asn	Gln	Asp	Ala	Asp	Arg	Gln	Glu	Leu
				245					250					255	
Val	Asn	Trp	Ala	Gln	Ala	Val	Gly	Gly	Pro	Ala	Ala	Ala	Phe	Asp	Phe
			260					265					270		
Thr	Thr	Lys	Gly	Val	Leu	Gln	Ala	Ala	Val	Gln	Gly	Glu	Leu	Trp	Arg
		275					280					285			
Met	Lys	Asp	Gly	Asn	Gly	Lys	Ala	Pro	Gly	Met	Ile	Gly	Trp	Leu	Pro
	290					295					300				
Glu	Lys	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gly	Ser	Thr	Gln
305					310					315					320
Asn	Ser	Trp	Pro	Phe	Pro	Ser	Asp	Lys	Val	Met	Gln	Gly	Tyr	Ala	Tyr
				325					330					335	
Ile	Leu	Thr	His	Pro	Gly	Thr	Pro	Cys	Ile	Phe	Tyr	Asp	His	Val	Phe
			340					345					350		
Asp	Trp	Asn	Leu	Lys	Gln	Glu	Ile	Ser	Ala	Leu	Ser	Ala	Val	Arg	Ser
		355					360					365			
Arg	Asn	Gly	Ile	His	Pro	Gly	Ser	Glu	Leu	Asn	Ile	Leu	Ala	Ala	Asp
	370					375					380				
Gly	Asp	Leu	Tyr	Val	Ala	Lys	Ile	Asp	Asp	Lys	Val	Ile	Val	Lys	Ile
385					390					395					400
Gly	Ser	Arg	Tyr	Asp	Val	Gly	Asn	Leu	Ile	Pro	Ser	Asp	Phe	His	Ala
				405					410					415	
Val	Ala	His	Gly	Asn	Asn	Tyr	Cys	Val	Trp	Glu	Lys	His	Gly	Leu	Arg
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Val Pro Ala Gly Arg His His
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<210> 52
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 52
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aagaagcaag gtgggtggta caactacctc ctggggcggg tggacgacat cgccgcgacg 180
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gtcgacagca ccgcccccac cttcgtcgtc gccgagatat ggagctccct ccactacgac 720
ggcaacggcg agccgtccag caaccaggac gccgacaggc aggagctggt caactgggcg 780
caggcggtgg gcggccccgc cgcggcgttc gacttcacca ccaagggcgt gctgcaggcg 840
gccgtccagg gcgagctgtg gcgcatgaag gacggcaacg gcaaggcgcc cgggatgatc 900
ggctggctgc cggagaaggc cgtcacgttc gtcgacaacc acgacaccgg ctccacgcag 960
aactcgtggc cattcccctc cgacaaggtc atgcagggct acgcctatat cctcacgcac 1020
ccaggaactc catgcatctt ctacgaccac gttttcgact ggaacctgaa gcaggagatc 1080
agcgcgctgt ctgcggtgag gtcaagaaac gggatccacc cggggagcga gctgaacatc 1140
ctcgccgccg acggggatct ctacgtcgcc aagattgacg acaaggtcat cgtgaagatc 1200
gggtcacggt acgacgtcgg gaacctgatc ccctcagact tccacgccgt tgcccctggc 1260
aacaactact gcgtttggga gaagcacggt ctgagagttc cagcggggcg gcaccactag 1320

<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 53
Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Thr Thr Gly Ser Gly Gly
1 5 10 15
Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser Thr
20 25 30
Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val
35 40 45

<210> 54
<211> 137
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 54
gccaccggcg gcaccaccac caccgccacc accaccggct ccggcggcgt gacctccacc 60
tccaagacca ccaccaccgc ctccaagacc tccaccacca cctcctccac ctcctgcacc 120
accccgaccg ccgtgtc 137

<210> 55
<211> 300
<212> PRT
<213> Pyrococcus furiosus

<400> 55
Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys Ser Thr Ser
1 5 10 15
Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr Thr Lys Val
20 25 30
Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly Ala Pro Ile
35 40 45
Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu Ile Asn Leu
50 55 60
Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr Tyr Asn Leu
65 70 75 80
Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn Ile Val Leu
85 90 95
Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile Phe Tyr Gly
100 105 110
Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro Ile Pro Leu
115 120 125
Pro Ser Lys Val Ser Asn Leu Thr Asp Phe Tyr Leu Thr Ile Ser Tyr
130 135 140
Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala Ile Glu Ser
145 150 155 160
Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn Ser Asp Glu
165 170 175
Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln Pro Ala Gly
180 185 190
Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn Gly Thr Pro
195 200 205
Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly Trp Glu Tyr
210 215 220
Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr Val Thr Ile
225 230 235 240
Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser Ser Leu Pro
245 250 255
Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly Thr Glu Phe
260 265 270
Gly Thr Pro Ser Thr Thr Ser Ala His Leu Glu Trp Trp Ile Thr Asn
275 280 285
Ile Thr Leu Thr Pro Leu Asp Arg Pro Leu Ile Ser
290 295 300

<210> 56
<211> 903
<212> DNA
<213> Pyrococcus furiosus

<400> 56
atctacttcg tggagaagta ccacacctcc gaggacaagt ccacctccaa cacctcctcc 60
accccgccgc agaccaccct ctccaccacc aaggtgctca agatccgcta cccggacgac 120
ggcgagtggc ccggcgcccc gatcgacaag gacggcgacg gcaacccgga gttctacatc 180
gagatcaacc tctggaacat cctcaacgcc accggcttcg ccgagatgac ctacaacctc 240
actagtggcg tgctccacta cgtgcagcag ctcgacaaca tcgtgctccg cgaccgctcc 300
aactgggtgc acggctaccc ggaaatcttc tacggcaaca agccgtggaa cgccaactac 360
gccaccgacg gcccgatccc gctcccgtcc aaggtgtcca acctcaccga cttctacctc 420
accatctcct acaagctcga gccgaagaac ggtctcccga tcaacttcgc catcgagtcc 480
tggctcaccc gcgaggcctg gcgcaccacc ggcatcaact ccgacgagca ggaggtgatg 540
atctggatct actacgacgg cctccagccc gcgggctcca aggtgaagga gatcgtggtg 600
ccgatcatcg tgaacggcac cccggtgaac gccaccttcg aggtgtggaa ggccaacatc 660
ggctgggagt acgtggcctt ccgcatcaag accccgatca aggagggcac cgtgaccatc 720
ccgtacggcg ccttcatctc cgtggccgcc aacatctcct ccctcccgaa ctacaccgag 780
aagtacctcg aggacgtgga gatcggcacc gagttcggca ccccgtccac cacctccgcc 840
cacctcgagt ggtggatcac caacatcacc ctcaccccgc tcgaccgccc gctcatctcc 900
tag 903

<210> 57
<211> 387
<212> PRT
<213> Thermus flavus

<400> 57
Met Tyr Glu Pro Lys Pro Glu His Arg Phe Thr Phe Gly Leu Trp Thr
1 5 10 15
Val Asp Asn Val Asp Arg Asp Pro Phe Gly Asp Thr Val Arg Glu Arg
20 25 30
Leu Asp Pro Val Tyr Val Val His Lys Leu Ala Glu Leu Gly Ala Tyr
35 40 45
Gly Val Asn Leu His Asp Glu Asp Leu Ile Pro Arg Gly Thr Pro Pro
50 55 60
Gln Glu Arg Asp Gln Ile Val Arg Arg Phe Lys Lys Ala Leu Asp Glu
65 70 75 80
Thr Val Leu Lys Val Pro Met Val Thr Ala Asn Leu Phe Ser Glu Pro
85 90 95
Ala Phe Arg Asp Gly Ala Ser Thr Thr Arg Asp Pro Trp Val Trp Ala
100 105 110
Tyr Ala Leu Arg Lys Ser Leu Glu Thr Met Asp Leu Gly Ala Glu Leu
115 120 125
Gly Ala Glu Ile Tyr Met Phe Trp Met Val Arg Glu Arg Ser Glu Val
130 135 140
Glu Ser Thr Asp Lys Thr Arg Lys Val Trp Asp Trp Val Arg Glu Thr
145 150 155 160
Leu Asn Phe Met Thr Ala Tyr Thr Glu Asp Gln Gly Tyr Gly Tyr Arg
165 170 175
Phe Ser Val Glu Pro Lys Pro Asn Glu Pro Arg Gly Asp Ile Tyr Phe
180 185 190
Thr Thr Val Gly Ser Met Leu Ala Leu Ile His Thr Leu Asp Arg Pro
195 200 205
Glu Arg Phe Gly Leu Asn Pro Glu Phe Ala His Glu Thr Met Ala Gly
210 215 220
Leu Asn Phe Asp His Ala Val Ala Gln Ala Val Asp Ala Gly Lys Leu
225 230 235 240
Phe His Ile Asp Leu Asn Asp Gln Arg Met Ser Arg Phe Asp Gln Asp
245 250 255
Leu Arg Phe Gly Ser Glu Asn Leu Lys Ala Gly Phe Phe Leu Val Asp
260 265 270

Leu Leu Glu Ser Ser Gly Tyr Gln Gly Pro Arg His Phe Glu Ala His
275 280 285
Ala Leu Arg Thr Glu Asp Glu Glu Gly Val Trp Thr Phe Val Arg Val
290 295 300
Cys Met Arg Thr Tyr Leu Ile Ile Lys Val Arg Ala Glu Thr Phe Arg
305 310 315 320
Glu Asp Pro Glu Val Lys Glu Leu Leu Ala Ala Tyr Tyr Gln Glu Asp
325 330 335
Pro Ala Thr Leu Ala Leu Leu Asp Pro Tyr Ser Arg Glu Lys Ala Glu
340 345 350
Ala Leu Lys Arg Ala Glu Leu Pro Leu Glu Thr Lys Arg Arg Arg Gly
355 360 365
Tyr Ala Leu Glu Arg Leu Asp Gln Leu Ala Val Glu Tyr Leu Leu Gly
370 375 380
Val Arg Gly
385

<210> 58
<211> 978
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 58
atggggaaga acggcaacct gtgctgcttc tctctgctgc tgcttcttct cgccgggttg 60
gcgtccggcc atcaaatcta cttcgtggag aagtaccaca cctccgagga caagtccacc 120
tccaacacct cctccacccc gccgcagacc accctctcca ccaccaaggt gctcaagatc 180
cgctacccgg acgacggtga gtggcccggc gccccgatcg acaaggacgg cgacggcaac 240
ccggagttct acatcgagat caacctctgg aacatcctca acgccaccgg cttcgccgag 300
atgacctaca acctcactag tggcgtgctc cactacgtgc agcagctcga caacatcgtg 360
ctccgcgacc gctccaactg ggtgcacggc tacccggaaa tcttctacgg caacaagccg 420
tggaacgcca actacgccac cgacggcccg atcccgctcc cgtccaaggt gtccaacctc 480
accgacttct acctcaccat ctcctacaag ctcgagccga agaacggtct cccgatcaac 540
ttcgccatcg agtcctggct cacccgcgag gcctggcgca ccaccggcat caactccgac 600
gagcaggagg tgatgatctg gatctactac gacggcctcc agcccgcggg ctccaaggtg 660
aaggagatcg tggtgccgat catcgtgaac ggcaccccgg tgaacgccac cttcgaggtg 720
tggaaggcca acatcggctg ggagtacgtg gccttccgca tcaagacccc gatcaaggag 780
ggcaccgtga ccatcccgta cggcgccttc atctccgtgg ccgccaacat ctcctccctc 840
ccgaactaca ccgagaagta cctcgaggac gtggagatcg gcaccgagtt cggcaccccg 900
tccaccacct ccgcccacct cgagtggtgg atcaccaaca tcaccctcac cccgctcgac 960
cgcccgctca tctcctag 978

<210> 59
<211> 1920
<212> DNA
<213> Aspergillus niger

<400> 59
atgtccttcc gctccctcct cgccctctcc ggcctcgtgt gcaccggcct cgccaacgtg 60
atctccaagc gcgccaccct cgactcctgg ctctccaacg aggccaccgt ggcccgcacc 120
gccatcctca acaacatcgg cgccgacggc gcctgggtgt ccggcgccga ctccggcatc 180
gtggtggcct ccccgtccac cgacaacccg gactacttct acacctggac ccgcgactcc 240
ggcctcgtgc tcaagaccct cgtggacctc ttccgcaacg gcgacacctc cctcctctcc 300
accatcgaga actacatctc cgcccaggcc atcgtgcagg gcatctccaa cccgtccggc 360
gacctctcct ccggcgccgg cctcggcgag ccgaagttca acgtggacga gaccgcctac 420

accggctcct ggggccgccc gcagcgcgac ggcccggccc tccgcgccac cgccatgatc 480
ggcttcggcc agtggctcct cgacaacggc tacacctcca ccgccaccga catcgtgtgg 540
ccgctcgtgc gcaacgacct ctcctacgtg gcccagtact ggaaccagac cggctacgac 600
ctctgggagg aggtgaacgg ctcctccttc ttcaccatcg ccgtgcagca ccgcgccctc 660
gtggagggct ccgccttcgc caccgccgtg ggctcctcct gctcctggtg cgactcccag 720
gccccggaga tcctctgcta cctccagtcc ttctggaccg gctccttcat cctcgccaac 780
ttcgactcct cccgctccgg caaggacgcc aacaccctcc tcggctccat ccacaccttc 840
gacccggagg ccgcctgcga cgactccacc ttccagccgt gctccccgcg cgccctcgcc 900
aaccacaagg aggtggtgga ctccttccgc tccatctaca ccctcaacga cggcctctcc 960
gactccgagg ccgtggccgt gggccgctac ccggaggaca cctactacaa cggcaacccg 1020
tggttcctct gcaccctcgc cgccgccgag cagctctacg acgccctcta ccagtgggac 1080
aagcagggct ccctcgaggt gaccgacgtg tccctcgact tcttcaaggc cctctactcc 1140
gacgccgcca ccggcaccta ctcctcctcc tcctccacct actcctccat cgtggacgcc 1200
gtgaagacct tcgccgacgg cttcgtgtcc atcgtggaga cccacgccgc ctccaacggc 1260
tccatgtccg agcagtacga caagtccgac ggcgagcagc tctccgcccg cgacctcacc 1320
tggtcctacg ccgccctcct caccgccaac aaccgccgca actccgtggt gccggcctcc 1380
tggggcgaga cctccgcctc ctccgtgccg ggcacctgcg ccgccacctc cgccatcggc 1440
acctactcct ccgtgaccgt gacctcctgg ccgtccatcg tggccaccgg cggcaccacc 1500
accaccgcca ccccgaccgg ctccggctcc gtgacctcca cctccaagac caccgccacc 1560
gcctccaaga cctccacctc cacctcctcc acctcctgca ccaccccgac cgccgtggcc 1620
gtgaccttcg acctcaccgc caccaccacc tacggcgaga acatctacct cgtgggctcc 1680
atctcccagc tcggcgactg ggagacctcc gacggcatcg ccctctccgc cgacaagtac 1740
acctcctccg acccgctctg gtacgtgacc gtgaccctcc cggccggcga gtccttcgag 1800
tacaagttca tccgcatcga gtccgacgac tccgtggagt gggagtccga cccgaaccgc 1860
gagtacaccg tgccgcaggc ctgcggcacc tccaccgcca ccgtgaccga cacctggcgc 1920

<210> 60
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 60
Ser Glu Lys Asp Glu Leu
1 5

<210> 61
<211> 561
<212> DNA
<213> Artificial Sequence

<220>
<223> Xylanase BD7436

<220>
<221> CDS
<222> (1)..(561)

<400> 61
atg gct agc acc ttc tac tgg cat ttg tgg acc gac ggc atc ggc acc 48
Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
1 5 10 15

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gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc        96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
            20                  25                  30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct       144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
        35                  40                  45

acc agg gtg atc aac tac aac gct cat gct ttc agc gtg gtg ggc aac       192
Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
    50                  55                  60

gct tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac       240
Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65                  70                  75                  80

tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag       288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
                85                  90                  95

ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc       336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
            100                 105                 110

agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa       384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
        115                 120                 125

ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc       432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
    130                 135                 140

atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac       480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145                 150                 155                 160

ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa       528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
                165                 170                 175

agc agc ggc tac agc aac gtg acc gtg tgg tag                           561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
            180                 185
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<210> 62
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 62

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Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
1               5                   10                  15
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Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
50 55 60

Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 63
<211> 561
<212> DNA
<213> Artificial Sequence

<220>
<223> Xylanase BD6002A

<220>
<221> CDS
<222> (1)..(561)

<400> 63
atg gct agc acc gac tac tgg caa aac tgg acc gac ggc ggc ggc acc 48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1 5 10 15

gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc 96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct 144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

acc agg gtg atc aac tac aac gct ggc gct ttc agc cca agc ggc aac 192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

ggc tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac 240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag 288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc 336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa 384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc 432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac 480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa 528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

agc agc ggc tac agc aac gtg acc gtg tgg tag 561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 64
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 64

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 65
<211> 561
<212> DNA
<213> Artificial Sequence

<220>
<223> Xylanase BD6002B

<220>
<221> CDS
<222> (1)..(561)

<400> 65

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atg gcc tcc acc gac tac tgg cag aac tgg acc gac ggc ggc ggc acc        48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1               5                  10                  15

gtg aac gcc acc aac ggc tcc gac ggc aac tac tcc gtg tcc tgg tcc        96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
            20                  25                  30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc tcc gcc       144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
        35                  40                  45

acc cgc gtg atc aac tac aac gcc ggc gcc ttc tcc ccg tcc ggc aac       192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
    50                  55                  60

ggc tac ctc gcc ctc tac ggc tgg acc cgc aac tcc ctc atc gag tac       240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65                  70                  75                  80

tac gtg gtg gac tcc tgg ggc acc tac cgc ccg acc ggc acc tac aag       288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
                85                  90                  95

ggc acc gtg acc tcc gac ggc ggc acc tac gac atc tac acc acc acc       336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
            100                 105                 110

cgc acc aac gcc ccg tcc atc gac ggc aac aac acc acc ttc acc cag       384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
        115                 120                 125

ttc tgg tcc gtg cgc cag tcc aag cgc ccg atc ggc acc aac aac acc       432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
    130                 135                 140

atc acc ttc tcc aac cac gtg aac gcc tgg aag tcc aag ggc atg aac       480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145                 150                 155                 160

ctc ggc tcc tcc tgg tcc tac cag gtg ctc gcc acc gag ggc tac cag       528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
                165                 170                 175

tcc tcc ggc tac tcc aac gtg acc gtg tgg tga                           561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
            180                 185
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<210> 66
<211> 186

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 66

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 67
<211> 2071

<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(2071)
<223> Promoter

<400> 67
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catttcggat catgatgtat gtgatttcca atctgctgca atatgaatgg agactctgtg 120

ctaaccatca acaacatgaa atgcttatga ggcctttgct gagcagccaa tcttgcctgt 180

gtttatgtct tcacaggccg aattcctctg ttttgttttt caccctcaat atttggaaac 240

atttatctag gttgtttgtg tccaggccta taaatcatac atgatgttgt cgtattggat 300

gtgaatgtgg tggcgtgttc agtgccttgg atttgagttt gatgagagtt gcttctgggt 360

caccactcac cattatcgat gctcctcttc agcataaggt aaaagtcttc cctgtttacg 420

ttattttacc cactatggtt gcttgggttg gttttttcct gattgcttat gccatggaaa 480

gtcatttgat atgttgaact tgaattaact gtagaattgt atacatgttc catttgtgtt 540

gtacttcctt cttttctatt agtagcctca gatgagtgtg aaaaaaacag attatataac 600

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catgagcaat agtgttgcaa tgatatttag gctgcattcg tttactctct tgatttccat 840

gagcacgctt cccaaactgt taaactctgt gtttttttgcc aaaaaaaaat gcataggaaa 900

gttgctttta aaaaatcata tcaatccatt ttttaagtta tagctaatac ttaattaatc 960

atgcgctaat aagtcactct gtttttcgta ctagagagat tgttttgaac cagcactcaa 1020

gaacacagcc ttaacccagc caaataatgc tacaacctac cagtccacac ctcttgtaaa 1080

gcatttgttg catggaaaag ctaagatgac agcaacctgt tcaggaaaac aactgacaag 1140

gtcataggga gagggagctt ttggaaaggt gccgtgcagt tcaaacaatt agttagcagt 1200

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caagataaag caaaatgatg tgtacataaa actccagagc tatatgtcat attgcaaaaa 1740

gaggagagct tataagacaa ggcatgactc acaaaaattc atttgccttt cgtgtcaaaa 1800

agaggagggc tttacattat ccatgtcata ttgcaaaaga aagagagaaa gaacaacaca 1860

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acacttcata tatcatgagt cacttcatgt ctggacatta acaaactcta tcttaacatt 1980

tagatgcaag agcctttatc tcactataaa tgcacgatga tttctcattg tttctcacaa 2040

aaagcattca gttcattagt cctacaacaa c 2071

<210> 68
<211> 79
<212> PRT
<213> Zea mays

<220>
<221> SIGNAL
<222> (1)..(79)
<223> Maize waxy signal sequence.

<400> 68

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala
65 70 75

<210> 69
<211> 1005

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Bromelain Sequence

<220>
<221> CDS
<222> (1)..(1005)
<223> Synthetic Bromelain

<400> 69

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atg gcc tgg aag gtg cag gtg gtg ttc ctc ttc ctc ttc ctc tgc gtg        48
Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1               5                   10                  15

atg tgg gcc tcc ccg tcc gcc gcc tcc gcg gac gag ccg tcc gac ccg        96
Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
            20                  25                  30

atg atg aag cgc ttc gag gag tgg atg gtg gag tac ggc cgc gtg tac       144
Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
        35                  40                  45

aag gac aac gac gag aag atg cgc cgc ttc cag atc ttc aag aac aac       192
Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
    50                  55                  60

gtg aac cac atc gag acc ttc aac tcc cgc aac gag aac tcc tac acc       240
Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
65                  70                  75                  80

ctc ggc atc aac cag ttc acc gac atg acc aac aac gag ttc atc gcc       288
Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
                85                  90                  95

cag tac acc ggc ggc atc tcc cgc ccg ctc aac atc gag cgc gag ccg       336
Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
            100                 105                 110

gtg gtg tcc ttc gac gac gtg gac atc tcc gcc gtg ccg cag tcc atc       384
Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
        115                 120                 125

gac tgg cgc gac tac ggc gcc gtg acc tcc gtg aag aac cag aac ccg       432
Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
    130                 135                 140

tgc ggc gcc tgc tgg gcc ttc gcc gcc atc gcc acc gtg gag tcc atc       480
Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
145                 150                 155                 160

tac aag atc aag aag ggc atc ctc gag ccg ctc tcc gag cag cag gtg       528
Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
                165                 170                 175

ctc gac tgc gcc aag ggc tac ggc tgc aag ggc ggc tgg gag ttc cgc       576
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Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
                180                 185                 190

gcc ttc gag ttc atc atc tcc aac aag ggc gtg gcc tcc ggc gcc atc      624
Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
        195                 200                 205

tac ccg tac aag gcc gcc aag ggc acc tgc aag acc gac ggc gtg ccg      672
Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
    210                 215                 220

aac tcc gcc tac atc acc ggc tac gcc cgc gtg ccg cgc aac aac gag      720
Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
225                 230                 235                 240

tcc tcc atg atg tac gcc gtg tcc aag cag ccg atc acc gtg gcc gtg      768
Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
                245                 250                 255

gac gcc aac gcc aac ttc cag tac tac aag tcc ggc gtg ttc aac ggc      816
Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
            260                 265                 270

ccg tgc ggc acc tcc ctc aac cac gcc gtg acc gcc atc ggc tac ggc      864
Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
        275                 280                 285

cag gac tcc atc atc tac ccg aag aag tgg ggc gcc aag tgg ggc gag      912
Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
    290                 295                 300

gcc ggc tac atc cgc atg gcc cgc gac gtg tcc tcc tcc tcc ggc atc      960
Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
305                 310                 315                 320

tgc ggc atc gcc atc gac ccg ctc tac ccg acc ctc gag gag tag         1005
Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
                325                 330
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<210> 70
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 70

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Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1               5                  10                  15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
            20                  25                  30
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Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
35 40 45

Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
50 55 60

Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
65 70 75 80

Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
85 90 95

Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
100 105 110

Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
115 120 125

Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
130 135 140

Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
145 150 155 160

Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
165 170 175

Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
180 185 190

Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
195 200 205

Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
210 215 220

Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
225 230 235 240

Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
245 250 255

Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
260 265 270

Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
275 280 285

Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
290 295 300

Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
305 310 315 320

Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
325 330

<210> 71
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Bromealin signal sequence

<400> 71
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ccgtccgccg cctccgcc 78

<210> 72
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Bromealin signal peptide

<400> 72

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala
20 25

<210> 73
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11000

<400> 73
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ccgtccgccg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg 120

atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180

ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctcctacacc 240

ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300

ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360

atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420

aaccagaacc cgtgcggcgc ctgctgggcc ttcgccgcca tcgccaccgt ggagtccatc 480

tacaagatca agaagggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540

aagggctacg gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600

aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660

gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgccgcg caacaacgag 720

tcctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780

aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac 840

gccgtgaccg ccatcggcta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900

aagtggggcg aggccggcta catccgcatg gcccgcgacg tgtcctcctc ctccggcatc 960

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gccgccaact ccaccctcgt ggccgagtag 1050

<210> 74
<211> 1067
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11589

<400> 74
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ccgaccgcgc cgcctccacc gacgagccgt ccgacccgat gatgaagcgc ttcgaggagt 180

ggatggtgga gtacggccgc gtgtacaagg acaacgacga gaagatgcgc cgcttccaga 240

tcttcaagaa caacgtgaac cacatcgaga ccttcaactc ccgcaacgag aactcctaca 300

ccctcggcat caaccagttc accgacatga ccaacaacga gttcatcgcc cagtacaccg 360

gcggcatctc ccgcccgctc aacatcgagc gcgagccggt ggtgtccttc gacgacgtgg 420

acatctccgc cgtgccgcag tccatcgact ggcgcgacta cggcgccgtg acctccgtga 480

agaaccagaa cccgtgcggc gcctgctggg ccttcgccgc catcgccacc gtggagtcca 540

tctacaagat caagaagggc atcctcgagc cgctctccga gcagcaggtg ctcgactgcg 600

ccaagggcta cggctgcaag ggcggctggg agttccgcgc cttcgagttc atcatctcca 660

acaagggcgt ggcctccggc gccatctacc cgtacaaggc cgccaagggc acctgcaaga 720

ccgacggcgt gccgaactcc gcctacatca ccggctacgc ccgcgtgccg cgcaacaacg 780

agtcctccat gatgtacgcc gtgtccaagc agccgatcac cgtggccgtg gacgccaacg 840

ccaacttcca gtactacaag tccggcgtgt tcaacggccc gtgcggcacc tccctcaacc 900

acgccgtgac cgccatcggc tacggccagg actccatcat ctacccgaag aagtggggcg 960

ccaagtgggg cgaggccggc tacatccgca tggcccgcga cgtgtcctcc tcctccggca 1020

tctgcggcat cgccatcgac ccgctctacc cgaccctcga ggagtag 1067

<210> 75
<211> 1023
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11587 Sequence

<400> 75
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ccgtccgccg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg 120

atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180

ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctcctacacc 240

ctcggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300

ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360

atctccgccg tgccgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420

aaccagaacc cgtgcggcgc ctgctgggcc ttcgccgcca tcgccaccgt ggagtccatc 480

tacaagatca agaagggcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540

aagggctacg gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600

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tcctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780

aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac 840

gccgtgaccg ccatcggcta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900

aagtggggcg aggccggcta catccgcatg gcccgcgacg tgtcctcctc ctccggcatc 960

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tag 1023

<210> 76
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN12169 Sequence

<400> 76
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gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggt ggagtacggc 120

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aaccacatcg agaccttcaa ctcccgcaac gagaactcct acaccctcgg catcaaccag 240

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aagtccggcg tgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc 840

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ggctacatcc gcatggcccg cgacgtgtcc tcctcctccg gcatctgcgg catcgccatc 960

gacccgctct acccgaccct cgaggagtag 990

<210> 77
<211> 1170
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN12575 Sequence

<400> 77
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gacgcgtcca cgttccgccg cggcgccgcg cagggcctga ggggggcccg ggcgtcggcg 120

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caggcgcgcc gcggggccag gttcccgtcg ctcgtcgtgt gcgccagcgc cggcgccatg 240

gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggt ggagtacggc 300

cgcgtgtaca aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg 360

aaccacatcg agaccttcaa ctcccgcaac gagaactcct acaccctcgg catcaaccag 420

ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcggcat ctcccgcccg 480

ctcaacatcg agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc cgccgtgccg 540

cagtccatcg actggcgcga ctacggcgcc gtgacctccg tgaagaacca gaacccgtgc 600

ggcgcctgct gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag 660

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aagggcggct gggagttccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc 780

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aagtccggcg tgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc 1020

ggctacggcc aggactccat catctacccg aagaagtggg gcgccaagtg gggcgaggcc 1080

ggctacatcc gcatggcccg cgacgtgtcc tcctcctccg gcatctgcgg catcgccatc 1140

gacccgctct acccgaccct cgaggagtag 1170

<210> 78
<211> 1068
<212> DNA
<213> Artificial Sequence

<220>
<223> pSM270 Sequence

<400> 78
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ccgtccgccg cctccgcctc ctcctcctcc ttcgccgact ccaacccgat ccgcccggtg 120

accgaccgcg ccgcctccac cgacgagccg tccgacccga tgatgaagcg cttcgaggag 180

tggatggtgg agtacggccg cgtgtacaag gacaacgacg agaagatgcg ccgcttccag 240

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accctcggca tcaaccagtt caccgacatg accaacaacg agttcatcgc ccagtacacc 360

ggcggcatct cccgcccgct caacatcgag cgcgagccgg tggtgtcctt cgacgacgtg 420

gacatctccg ccgtgccgca gtccatcgac tggcgcgact acggcgccgt gacctccgtg 480

aagaaccaga acccgtgcgg cgcctgctgg gccttcgccg ccatcgccac cgtggagtcc 540

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gccaagggct acggctgcaa gggcggctgg gagttccgcg ccttcgagtt catcatctcc 660

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cacgccgtga ccgccatcgg ctacggccag gactccatca tctacccgaa gaagtggggc 960

gccaagtggg gcgaggccgg ctacatccgc atggcccgcg acgtgtcctc ctcctccggc 1020

atctgcggca tcgccatcga cccgctctac ccgaccctcg aggagtag 1068

<210> 79
<211> 1497
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1497)
<223> Trichoderma reesei cellobiohyrodlase I

<400> 79
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Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1 5 10 15

tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc 96
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

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gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc      144
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
        35                  40                  45

acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac      192
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
    50                  55                  60

aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg      240
Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
65                  70                  75                  80

tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt      288
Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
                85                  90                  95

gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg      336
Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
            100                 105                 110

gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc      384
Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
        115                 120                 125

tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct      432
Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
    130                 135                 140

ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc      480
Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
145                 150                 155                 160

acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag      528
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
                165                 170                 175

tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc      576
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
            180                 185                 190

tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga      624
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
        195                 200                 205

agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag      672
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
    210                 215                 220

gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag      720
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
225                 230                 235                 240

ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act      768
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
                245                 250                 255

tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc      816
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
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                260                 265                 270

agc ttc tac ggc cct ggc tct agc ttt acc ctc gat acc acc aag aaa      864
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
        275                 280                 285

ttg acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac cga tac      912
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
    290                 295                 300

tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt      960
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
305                 310                 315                 320

agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag     1008
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
                325                 330                 335

gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag     1056
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
            340                 345                 350

ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg     1104
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
        355                 360                 365

gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca     1152
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
    370                 375                 380

aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc     1200
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
385                 390                 395                 400

agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag     1248
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
                405                 410                 415

gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac     1296
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
            420                 425                 430

cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc     1344
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
        435                 440                 445

acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag     1392
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
    450                 455                 460

tct cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc acg gtc     1440
Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465                 470                 475                 480

tgc gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac tct cag     1488
Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
                485                 490                 495
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tgc ctg taa 1497
Cys Leu

<210> 80
<211> 498
<212> PRT
<213> Trichoderma reesei

<400> 80

Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1 5 10 15

Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
35 40 45

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
50 55 60

Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
65 70 75 80

Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
85 90 95

Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
100 105 110

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
115 120 125

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
130 135 140

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
145 150 155 160

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
165 170 175

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
180 185 190

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
195 200 205

Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
210 215 220

Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
225 230 235 240

Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
245 250 255

Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
260 265 270

Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
275 280 285

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
290 295 300

Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
305 310 315 320

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
325 330 335

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
340 345 350

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
355 360 365

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
370 375 380

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
385 390 395 400

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
405 410 415

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
420 425 430

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
435 440 445

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
450 455 460

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465 470 475 480

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
485 490 495

Cys Leu

<210> 81
<211> 1365
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1365)
<223> trichoderma reesei cellobiohydrolase II

<400> 81
atg gtg cct cta gag gag cgg caa gct tgc tca agc gtc tgg ggc caa 48
Met Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly Gln
1 5 10 15

tgt ggt ggc cag aat tgg tcg ggt ccg act tgc tgt gct tcc gga agc 96
Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
20 25 30

aca tgc gtc tac tcc aac gac tat tac tcc cag tgt ctt ccc ggc gct 144
Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
35 40 45

gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg act tca cga gta 192
Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
50 55 60

tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct cca cct ggt tct 240
Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
65 70 75 80

acc act acc aga gta cct cca gtc gga tcg gga acc gct acg tat tca 288
Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser

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                    85                  90                  95

ggc aac cct ttt gtt ggg gtc act cct tgg gcc aat gca tat tac gcc      336
Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
            100                 105                 110

tct gaa gtt agc agc ctc gct att cct agc ttg act gga gcc atg gcc      384
Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
        115                 120                 125

act gct gca gca gct gtc gca aag gtt ccc tct ttt atg tgg cta gat      432
Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
    130                 135                 140

act ctt gac aag acc cct ctc atg gag caa acc ttg gcc gac atc cgc      480
Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
145                 150                 155                 160

acc gcc aac aag aat ggc ggt aac tat gcc gga cag ttt gtg gtg tat      528
Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
                165                 170                 175

gac ttg ccg gat cgc gat tgc gct gcc ctt gcc tcg aat ggc gaa tac      576
Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
            180                 185                 190

tct att gcc gat ggt ggc gtc gcc aaa tat aag aac tat atc gac acc      624
Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
        195                 200                 205

att cgt caa att gtc gtg gaa tat tcc gat atc cgg acc ctc ctg gtt      672
Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
    210                 215                 220

att gag cct gac tct ctt gcc aac ctg gtg acc aac ctc ggt act cca      720
Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
225                 230                 235                 240

aag tgt gcc aat gct cag tca gcc tac ctt gag tgc atc aac tac gcc      768
Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
                245                 250                 255

gtc aca cag ctg aac ctt cca aat gtt gcg atg tat ttg gac gct ggc      816
Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
            260                 265                 270

cat gca gga tgg ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag      864
His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
        275                 280                 285

cta ttt gca aat gtt tac aag aat gca tcg tct ccg aga gct ctt cgc      912
Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
    290                 295                 300

gga ttg gca acc aat gtc gcc aac tac aac ggg tgg aac att acc agc      960
Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
305                 310                 315                 320
```

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ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag aag ctg tac      1008
Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
                325                 330                 335

atc cac gct att gga cct ctt ctt gcc aat cac ggc tgg tcc aac gcc      1056
Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
            340                 345                 350

ttc ttc atc act gat caa ggt cga tcg gga aag cag cct acc gga cag      1104
Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
        355                 360                 365

caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt ggt att      1152
Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
    370                 375                 380

cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg      1200
Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
385                 390                 395                 400

gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc agt gcg cca      1248
Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
                405                 410                 415

cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg gcg cct      1296
Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
            420                 425                 430

caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac      1344
Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
        435                 440                 445

gca aac cca tcg ttc ctg tag                                         1365
Ala Asn Pro Ser Phe Leu
    450
```

<210> 82
<211> 454
<212> PRT
<213> Trichoderma reesei

<400> 82

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Met Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly Gln
1               5                   10                  15

Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
            20                  25                  30

Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
        35                  40                  45

Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
    50                  55                  60
```

Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
65 70 75 80

Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser
85 90 95

Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
100 105 110

Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
115 120 125

Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
130 135 140

Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
145 150 155 160

Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
165 170 175

Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
180 185 190

Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
195 200 205

Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
210 215 220

Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
225 230 235 240

Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
245 250 255

Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
260 265 270

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
275 280 285

Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
290 295 300

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
305 310 315 320

Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
325 330 335

Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
340 345 350

Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
355 360 365

Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
370 375 380

Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
385 390 395 400

Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
405 410 415

Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
420 425 430

Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
435 440 445

Ala Asn Pro Ser Phe Leu
450

<210> 83
<211> 1317
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1317)
<223> Trichoderma reesei endoglucanase I

<400> 83
atg cag caa ccg gga acc agc acc ccc gag gtc cat ccc aag ttg aca 48
Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr

```
1               5                   10                  15

acc tac aag tgc aca aag tcc ggg ggg tgc gtg gcc cag gac acc tcg      96
Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
            20                  25                  30

gtg gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac tac aac     144
Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
        35                  40                  45

tcg tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct gac gag     192
Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
    50                  55                  60

gcg acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac gcc gcc     240
Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
65                  70                  75                  80

tcg ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag tac atg     288
Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
                85                  90                  95

ccc agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg tat ctc     336
Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
            100                 105                 110

ctg gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc cag gag     384
Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
        115                 120                 125

ctg agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag aac ggc     432
Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
    130                 135                 140

tcg ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac cag tat     480
Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
145                 150                 155                 160

aac acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct cag tgc     528
Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
                165                 170                 175

ccc gtc cag aca tgg agg aac ggc acc ctc aac act agc cac cag ggc     576
Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
            180                 185                 190

ttc tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg gcg aat     624
Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
        195                 200                 205

gcc ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct gcc ggt     672
Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
    210                 215                 220

tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc     720
Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
225                 230                 235                 240
```

```
gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc      768
Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
                245                 250                 255

aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc      816
Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
            260                 265                 270

aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc      864
Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
        275                 280                 285

gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc      912
Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
    290                 295                 300

acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att      960
Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
305                 310                 315                 320

tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc     1008
Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
                325                 330                 335

ggc ccc tgc agc agc acc gag ggc aac cca tcc aac acc ctg gcc aac     1056
Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
            340                 345                 350

aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att     1104
Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
        355                 360                 365

ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc     1152
Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
    370                 375                 380

acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg     1200
Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
385                 390                 395                 400

agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc     1248
Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
                405                 410                 415

ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac     1296
Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
            420                 425                 430

tac tac tcg caa tgc ctt tag                                        1317
Tyr Tyr Ser Gln Cys Leu
        435
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<210> 84
<211> 438
<212> PRT
<213> Trichoderma reesei

<400> 84

Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
1 5 10 15

Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
20 25 30

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
35 40 45

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
50 55 60

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
65 70 75 80

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
85 90 95

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
100 105 110

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
115 120 125

Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
130 135 140

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
145 150 155 160

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
165 170 175

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
180 185 190

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
195 200 205

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
210 215 220

```
Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
225                 230                 235                 240

Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
                245                 250                 255

Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
            260                 265                 270

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
        275                 280                 285

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
    290                 295                 300

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
305                 310                 315                 320

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
                325                 330                 335

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
            340                 345                 350

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
        355                 360                 365

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
    370                 375                 380

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
385                 390                 395                 400

Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
                405                 410                 415

Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
            420                 425                 430

Tyr Tyr Ser Gln Cys Leu
        435

<210>  85
<211>  954
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<212> DNA
<213> Artificial Sequence

<220>
<223> 6GP1

<220>
<221> CDS
<222> (1)..(954)
<223> 6GP1

<400> 85

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atg ggc gtg gac ccg ttc gag cgc aac aag atc ctc ggc cgc ggc atc        48
Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile
1               5                  10                  15

aac atc ggc aac gcc ctg gag gcc ccg aac gag ggc gac tgg ggc gtg        96
Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
            20                  25                  30

gtg atc aag gac gag ttc ttc gac atc atc aag gag gcc ggc ttc tcc       144
Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
        35                  40                  45

cac gtg cgc atc ccg atc cgc tgg tcc acc cac gcc tac gcc ttc ccg       192
His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
    50                  55                  60

ccg tac aag atc atg gac cgc ttc ttc aag cgc gtg gac gag gtg atc       240
Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
65                  70                  75                  80

aac ggc gcc ctc aag cgc ggc ctc gcc gtg gcc atc aac atc cac cac       288
Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
                85                  90                  95

tac gag gag ctc atg aac gac ccg gag gag cac aag gag cgc ttc ctc       336
Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
            100                 105                 110

gcc ctc tgg aag cag atc gcc gac cgc tac aag gac tac ccg gag acc       384
Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
        115                 120                 125

ctc ttc ttc gag atc ctc aac gag ccg cac ggc aac ctc acc ccg gag       432
Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
    130                 135                 140

aag tgg aac gag ctg ctc gag gag gcc ctc aag gtg atc cgc tcc atc       480
Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
145                 150                 155                 160

gac aag aag cac acc atc atc att ggc acc gca gag tgg gga ggc atc       528
Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
                165                 170                 175

tcc gcc ctc gag aag ctc tcc gtg ccg aag tgg gag aag aat tcc atc       576
```

```
Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
                180                 185                 190

gtg acc atc cac tac tac aac ccg ttc gag ttc acg cac cag ggc gcc      624
Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
        195                 200                 205

gag tgg gtg gag ggc tcc gag aag tgg ctt ggc cgc aag tgg ggc tcc      672
Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
    210                 215                 220

ccg gac gac cag aag cac ctc atc gag gag ttc aac ttc atc gag gag      720
Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
225                 230                 235                 240

tgg tcc aag aag aac aag cgc ccg atc tac atc ggc gag ttt ggc gcc      768
Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
                245                 250                 255

tac cgc aag gcc gac ctc gag tcc cgc atc aag tgg acc tcc ttc gtg      816
Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
            260                 265                 270

gtg cgt gag atg gag aag cgc cgc tgg tcc tgg gcc tac tgg gag ttc      864
Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
        275                 280                 285

tgc tcc ggc ttc ggc gtg tac gac acc ctc cgc aag acc tgg aac aag      912
Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
    290                 295                 300

gac ctc ctc gag gcc ctc atc ggc ggc gac tcc atc gag tag              954
Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
305                 310                 315
```

<210> 86
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 86

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Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile
1               5                  10                  15

Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
            20                  25                  30

Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
        35                  40                  45
```

```
His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
    50                  55                  60

Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
65                  70                  75                  80

Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
                85                  90                  95

Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
            100                 105                 110

Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
        115                 120                 125

Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
    130                 135                 140

Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
145                 150                 155                 160

Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
                165                 170                 175

Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
            180                 185                 190

Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
        195                 200                 205

Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
    210                 215                 220

Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
225                 230                 235                 240

Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
                245                 250                 255

Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
            260                 265                 270

Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
        275                 280                 285
```

Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
290 295 300

Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
305 310 315

<210> 87
<211> 1248
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(1248)
<223> Barley AmyI amylase

<400> 87

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atg gca cac caa gtc ctc ttt cag ggg ttc aac tgg gag tcg tgg aag        48
Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
1               5                   10                  15

cag agc ggc ggg tgg tac aac atg atg atg ggc aag gtc gac gac atc        96
Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
            20                  25                  30

gcc gct gcc gga gtc acc cac gtc tgg ctg cca ccg ccg tcg cac tcc       144
Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
        35                  40                  45

gtc tcc aac gaa ggt tac atg cct ggt cgg ctg tac gac atc gac gcg       192
Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
    50                  55                  60

tcc aag tac ggc aac gcg gcg gag ctc aag tcg ctc atc ggc gcg ctc       240
Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
65                  70                  75                  80

cac ggc aag ggc gtg cag gcc atc gcc gac atc gtc atc aac cac cgc       288
His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
                85                  90                  95

tgc gcc gac tac aag gat agc cgc ggc atc tac tgc atc ttc gag ggc       336
Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
            100                 105                 110

ggc acc tcc gac ggc cgc ctc gac tgg ggc ccc cac atg atc tgt cgc       384
Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
        115                 120                 125

gac gac acc aaa tac tcc gat ggc acc gca aac ctc gac acc gga gcc       432
Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
    130                 135                 140
```

```
gac ttc gcc gcc gcg ccc gac atc gac cac ctc aac gac cgg gtc cag      480
Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
145                 150                 155                 160

cgc gag ctc aag gag tgg ctc ctc tgg ctc aag agc gac ctc ggc ttc      528
Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
                165                 170                 175

gac gcg tgg cgc ctt gac ttc gcc agg ggc tac tcg ccg gag atg gcc      576
Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
            180                 185                 190

aag gtg tac atc gac ggc aca tcc ccg agc ctc gcc gtg gcc gag gtg      624
Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
        195                 200                 205

tgg gac aat atg gcc acc ggc ggc gac ggc aag ccc aac tac gac cag      672
Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
    210                 215                 220

gac gcg cac cgg cag aat ctg gtg aac tgg gtg gac aag gtg ggc ggc      720
Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
225                 230                 235                 240

gcg gcc tcg gca ggc atg gtg ttc gac ttc acg acc aaa ggg ata ctg      768
Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
                245                 250                 255

aac gct gcc gtg gag ggc gag ctg tgg agg ctg atc gac ccg cag ggg      816
Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
            260                 265                 270

aag gcc ccc ggc gtg atg gga tgg tgg ccg gcc aag gcc gtc acc ttc      864
Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
        275                 280                 285

gtc gac aac cac gat aca ggc tcc acg cag gcc atg tgg cca ttc ccc      912
Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
    290                 295                 300

tcc gac aag gtc atg cag ggc tac gcg tac atc ctc acc cac ccc ggc      960
Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
305                 310                 315                 320

atc cca tgc atc ttc tac gac cat ttc ttc aac tgg ggg ttt aag gac     1008
Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
                325                 330                 335

cag atc gcg gcg ctg gtg gcg atc agg aag cgc aac ggc atc acg gcg     1056
Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
            340                 345                 350

acg agc gct ctg aag atc ctc atg cac gaa gga gat gcc tac gtc gcc     1104
Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
        355                 360                 365

gag ata gac ggc aag gtg gtg gtg aag atc ggg tcc agg tac gac gtc     1152
Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
```

370 375 380

ggg gcg gtg atc ccg gcc ggg ttc gtg acc tcg gca cac ggc aac gac 1200
Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
385 390 395 400

tac gcc gtc tgg gag aag aac ggt gcc gcg gca aca cta caa cgg agc 1248
Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Thr Leu Gln Arg Ser
405 410 415

<210> 88
<211> 416
<212> PRT
<213> Hordeum vulgare

<400> 88

Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
1 5 10 15

Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
20 25 30

Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
35 40 45

Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
50 55 60

Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
65 70 75 80

His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
85 90 95

Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
100 105 110

Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
115 120 125

Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
130 135 140

Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
145 150 155 160

Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
165 170 175

Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
180 185 190

Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
195 200 205

Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
210 215 220

Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
225 230 235 240

Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
245 250 255

Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
260 265 270

Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
275 280 285

Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
290 295 300

Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
305 310 315 320

Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
325 330 335

Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
340 345 350

Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
355 360 365

Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
370 375 380

Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
385 390 395 400

Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
405 410 415

<210> 89
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Trichoderma reesei ß-Glucosidase 2

<220>
<221> CDS
<222> (1)..(1401)
<223> Trichoderma reesei ß-Glucosidase 2

<400> 89
atg ttg ccc aag gac ttt cag tgg ggg ttc gcc acg gct gcc tac cag 48
Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
1 5 10 15

atc gag ggc gcc gtc gac cag gac ggc cgc ggc ccc agc atc tgg gac 96
Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
20 25 30

acg ttc tgc gcg cag ccc ggc aag atc gcc gac ggc tcg tcg ggc gtg 144
Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
35 40 45

acg gcg tgc gac tcg tac aac cgc acg gcc gag gac att gcg ctg ctg 192
Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
50 55 60

aag tcg ctc ggg gcc aag agc tac cgc ttc tcc atc tcg tgg tcg cgc 240
Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65 70 75 80

atc atc ccc gag ggc ggc cgc ggc gat gcc gtc aac cag gcg ggc atc 288
Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
85 90 95

gac cac tac gtc aag ttc gtc gac gac ctg ctc gac gcc ggc atc acg 336
Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
100 105 110

ccc ttc atc acc ctc ttc cac tgg gac ctg ccc gag ggc ctg cat cag 384
Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
115 120 125

cgg tac ggg ggg ctg ctg aac cgc acc gag ttc ccg ctc gac ttt gaa 432
Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
130 135 140

aac tac gcc cgc gtc atg ttc agg gcg ctg ccc aag gtg cgc aac tgg 480

```
Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145                 150                 155                 160

atc acc ttc aac gag ccg ctg tgc tcg gcc atc ccg ggc tac ggc tcc      528
Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
                165                 170                 175

ggc acc ttc gcc ccc ggc cgg cag agc acc tcg gag ccg tgg acc gtc      576
Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
            180                 185                 190

ggc cac aac atc ctc gtc gcc cac ggc cgc gcc gtc aag gcg tac cgc      624
Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
        195                 200                 205

gac gac ttc aag ccc gcc agc ggc gac ggc cag atc ggc atc gtc ctc      672
Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
    210                 215                 220

aac ggc gac ttc acc tac ccc tgg gac gcc gcc gac ccg gcc gac aag      720
Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225                 230                 235                 240

gag gcg gcc gag cgg cgc ctc gag ttc ttc acg gcc tgg ttc gcg gac      768
Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
                245                 250                 255

ccc atc tac ttg ggc gac tac ccg gcg tcg atg cgc aag cag ctg ggc      816
Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
            260                 265                 270

gac cgg ctg ccg acc ttt acg ccc gag gag cgc gcc ctc gtc cac ggc      864
Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
        275                 280                 285

tcc aac gac ttt tac ggc atg aac cac tac acg tcc aac tac atc cgc      912
Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
    290                 295                 300

cac cgc agc tcg ccc gcc tcc gcc gac gac acc gtc ggc aac gtc gac      960
His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305                 310                 315                 320

gtg ctc ttc acc aac aag cag ggc aac tgc atc ggc ccc gag acg cag     1008
Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
                325                 330                 335

tcc ccc tgg ctg cgc ccc tgt gcc gcc ggc ttc cgc gac ttc ctg gtg     1056
Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
            340                 345                 350

tgg atc agc aag agg tac ggc tac ccg ccc atc tac gtg acg gag aac     1104
Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
        355                 360                 365

ggc acg agc atc aag ggc gag agc gac ttg ccc aag gag aag att ctc     1152
Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
    370                 375                 380
```

```
gaa gat gac ttc agg gtc aag tac tat aac gag tac atc cgt gcc atg      1200
Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385                 390                 395                 400

gtt acc gcc gtg gag ctg gac ggg gtc aac gtc aag ggg tac ttt gcc      1248
Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
                405                 410                 415

tgg tcg ctc atg gac aac ttt gag tgg gcg gac ggc tac gtg acg agg      1296
Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
            420                 425                 430

ttt ggg gtt acg tat gtg gat tat gag aat ggg cag aag cgg ttc ccc      1344
Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
        435                 440                 445

aag aag agc gca aag agc ttg aag ccg ctg ttt gac gag ctg att gcg      1392
Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
    450                 455                 460

gcg gcg tga                                                         1401
Ala Ala
465
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<210> 90
<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 90

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Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
1               5                   10                  15

Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
            20                  25                  30

Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
        35                  40                  45

Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
    50                  55                  60

Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65                  70                  75                  80

Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
                85                  90                  95
```

```
Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
               100                 105                 110

Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
           115                 120                 125

Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
       130                 135                 140

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145                 150                 155                 160

Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
                165                 170                 175

Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
            180                 185                 190

Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
        195                 200                 205

Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
    210                 215                 220

Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225                 230                 235                 240

Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
                245                 250                 255

Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
            260                 265                 270

Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
        275                 280                 285

Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
    290                 295                 300

His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305                 310                 315                 320
```

Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
325 330 335

Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
340 345 350

Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
355 360 365

Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
370 375 380

Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385 390 395 400

Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
405 410 415

Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
420 425 430

Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
435 440 445

Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
450 455 460

Ala Ala
465

<210> 91
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> Trichoderma reesei ß-Glucosidase D

<220>
<221> CDS
<222> (1)..(2103)
<223> Trichoderma reesei ß-Glucosidase D

<400> 91
atg att ctc ggc tgt gaa agc aca ggt gtc atc tct gcc gtc aaa cac 48
Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
1 5 10 15

```
ttt gtc gcc aac gac cag gag cac gag cgg cga gcg gtc gac tgt ctc        96
Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
            20                  25                  30

atc acc cag cgg gct ctc cgg gag gtc tat ctg cga ccc ttc cag atc       144
Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
        35                  40                  45

gta gcc cga gat gca agg ccc ggc gca ttg atg aca tcc tac aac aag       192
Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
    50                  55                  60

gtc aat ggc aag cac gtc gct gac agc gcc gag ttc ctt cag ggc att       240
Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
65                  70                  75                  80

ctc cgg act gag tgg aat tgg gac cct ctc att gtc agc gac tgg tac       288
Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
                85                  90                  95

ggc acc tac acc act att gat gcc atc aaa gcc ggc ctt gat ctc gag       336
Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
            100                 105                 110

atg ccg ggc gtt tca cga tat cgc ggc aaa tac atc gag tct gct ctg       384
Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
        115                 120                 125

cag gcc cgt ttg ctg aag cag tcc act atc gat gag cgc gct cgc cgc       432
Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
    130                 135                 140

gtg ctc agg ttc gcc cag aag gcc agc cat ctc aag gtc tcc gag gta       480
Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
145                 150                 155                 160

gag caa ggc cgt gac ttc cca gag gat cgc gtc ctc aac cgt cag atc       528
Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
                165                 170                 175

tgc ggc agc agc att gtc cta ctg aag aat gag aac tcc atc tta cct       576
Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
            180                 185                 190

ctc ccc aag tcc gtc aag aag gtc gcc ctt gtt ggt tcc cac gtg cgt       624
Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
        195                 200                 205

cta ccg gct atc tcg gga gga ggc agc gcc tct ctt gtc cct tac tat       672
Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
    210                 215                 220

gcc ata tct cta tac gat gcc gtc tct gag gta cta gcc ggt gcc acg       720
Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
225                 230                 235                 240

atc acg cac gag gtc ggt gcc tat gcc cac caa atg ctg ccc gtc atc       768
```

```
Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
                245                 250                 255

gac gca atg atc agc aac gcc gta atc cac ttc tac aac gac ccc atc      816
Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
            260                 265                 270

gat gtc aaa gac aga aag ctc ctt ggc agt gag aac gta tcg tcg aca      864
Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
        275                 280                 285

tcg ttc cag ctc atg gat tac aac aac atc cca acg ctc aac aag gcc      912
Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
    290                 295                 300

atg ttc tgg ggt act ctc gtg ggc gag ttt atc cct acc gcc acg gga      960
Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305                 310                 315                 320

att tgg gaa ttt ggc ctc agt gtc ttt ggc act gcc gac ctt tat att     1008
Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
                325                 330                 335

gat aat gag ctc gtg att gaa aat aca aca cat cag acg cgt gga acc     1056
Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
            340                 345                 350

gcc ttt ttc gga aag gga acg acg gaa aaa gtc gct acc agg agg atg     1104
Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
        355                 360                 365

gtg gcc ggc agc acc tac aag ctg cgt ctc gag ttt ggg tct gcc aac     1152
Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
    370                 375                 380

acg acc aag atg gag acg acc ggt gtt gtc aac ttt ggc ggc ggt gcc     1200
Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385                 390                 395                 400

gta cac ctg ggt gcc tgt ctc aag gtc gac cca cag gag atg att gcg     1248
Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
                405                 410                 415

cgg gcc gtc aag gcc gca gcc gat gcc gac tac acc atc atc tgc acg     1296
Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
            420                 425                 430

gga ctc agc ggc gag tgg gag tct gag ggt ttt gac cgg cct cac atg     1344
Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
        435                 440                 445

gac ctg ccc cct ggt gtg gac acc atg atc tcg caa gtt ctt gac gcc     1392
Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
    450                 455                 460

gct ccc aat gct gta gtc gtc aac cag tca ggc acc cca gtg aca atg     1440
Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465                 470                 475                 480
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agc tgg gct cat aaa gca aag gcc att gtg cag gct tgg tat ggt ggt      1488
Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
                485                 490                 495

aac gag aca ggc cac gga atc tcc gat gtg ctc ttt ggc aac gtc aac      1536
Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
            500                 505                 510

ccg tcg ggg aaa ctc tcc cta tcg tgg cca gtc gat gtg aag cac aac      1584
Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
        515                 520                 525

cca gca tat ctc aac tac gcc agc gtt ggt gga cgg gtc ttg tat ggc      1632
Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
    530                 535                 540

gag gat gtt tac gtt ggc tac aag ttc tac gac aaa acg gag agg gag      1680
Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545                 550                 555                 560

gtt ctg ttt cct ttt ggg cat ggc ctg tct tac gct acc ttc aag ctc      1728
Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
                565                 570                 575

cca gat tct acc gtg agg acg gtc ccc gaa acc ttc cac ccg gac cag      1776
Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
            580                 585                 590

ccc aca gta gcc att gtc aag atc aag aac acg agc agt gtc ccg ggc      1824
Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
        595                 600                 605

gcc cag gtc ctg cag tta tac att tcg gcc cca aac tcg cct aca cat      1872
Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
    610                 615                 620

cgc ccg gtc aag gag ctg cac gga ttc gaa aag gtg tat ctt gaa gct      1920
Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625                 630                 635                 640

ggc gag gag aag gag gta caa ata ccc att gac cag tac gct act agc      1968
Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
                645                 650                 655

ttc tgg gac gag att gag agc atg tgg aag agc gag agg ggc att tat      2016
Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr
            660                 665                 670

gat gtg ctt gta gga ttc tcg agt cag gaa atc tcg ggc aag ggg aag      2064
Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
        675                 680                 685

ctg att gtg cct gaa acg cga ttc tgg atg ggg ctg tag                  2103
Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
    690                 695                 700
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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 92

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Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
20 25 30

Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
35 40 45

Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
50 55 60

Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
65 70 75 80

Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
85 90 95

Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
100 105 110

Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
115 120 125

Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
130 135 140

Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
145 150 155 160

Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
165 170 175

Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
180 185 190

Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
195 200 205

Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
210 215 220

Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
225 230 235 240

Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
245 250 255

Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
260 265 270

Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
275 280 285

Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
290 295 300

Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
305 310 315 320

Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
325 330 335

Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
340 345 350

Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
355 360 365

Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
370 375 380

Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
385 390 395 400

Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
405 410 415

Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
420 425 430

Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
435 440 445

Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
450 455 460

Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
465 470 475 480

Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
485 490 495

Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
500 505 510

Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
515 520 525

Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
530 535 540

Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
545 550 555 560

Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
565 570 575

Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
580 585 590

Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
595 600 605

Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
610 615 620

Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
625 630 635 640

Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
645 650 655

Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly-Ile Tyr
660 665 670

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
675 680 685

Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
690 695 700

<210> 93
<211> 1496
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized CBHI

<400> 93
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ggacccacgc caccaactcc tccaccaact gctacgacgg caacacctgg tcctccaccc 180

tctgcccgga caacgagacc tgcgccaaga actgctgcct cgacggcgcc gcctacgcct 240

ccacctacgg cgtgaccacc tccggcaact ccctctccat cggcttcgtg acccagtccg 300

cccagaagaa cgtgggcgcc cgcctctacc tcatggcctc cgacaccacc taccaggagt 360

tcaccctcct cggcaacgag ttctccttcg acgtggacgt gtcccagctc ccgtgcggcc 420

tcaacggcgc cctctacttc gtgtccatgg acgccgacgg cggcgtgtcc aagtacccga 480

ccaacaccgc cggcgccaag tacggcaccg gctactgcga ctcccagtgc ccgcgcgacc 540

tcaagttcat caacggccag gccaacgtgg agggctggga gccgtcctcc aacaacgcca 600

acaccggcat cggcggccac ggctcctgct gctccgagat ggacatctgg gaggccaact 660

ccatctccga ggccctcacc ccgcacccgt gcaccaccgt gggccaggag atctgcgagg 720

gcgacggctg cggcggcacc tactccgaca accgctacgg cggcacctgc gacccggacg 780

gctgcgactg gaacccgtac cgcctcggca acacctcctt ctacggcccg ggctcctcct 840

tcaccctcga caccaccaag aagctcaccg tggtgaccca gttcgagacc tccggcgcca 900

tcaaccgcta ctacgtgcag aacggcgtga ccttccagca gccgaacgcc gagctcggct 960

cctactccgg caacgagctc aacgacgact actgcaccgc cgaggaggcc gagttcggcg 1020

gctcctcctt ctccgacaag ggcggcctca cccagttcaa gaaggccacc tccggcggca 1080

tggtgctcgt gatgtccctc tgggacgact actacgccaa catgctctgg ctcgactcca 1140

cctacccgac caacgagacc tcctccaccc cgggcgccgt gcgcggctcc tgctccacct 1200

cctccggcgt gccggcccag gtggagtccc agtccccgaa cgccaaggtg accttctcca 1260

acatcaagtt cggcccgatc ggctccaccg gcaacccgtc cggcggcaac ccgccgggcg 1320

gcaacccgcc gggcaccacc accacccgcc gcccggccac caccaccggc tcctccccgg 1380

gcccgaccca gtcccactac ggccagtgcg gcggcatcgg ctactccggc ccgaccgtgt 1440

gcgcctccgg caccacctgc caggtgctca acccgtacta ctcccagtgc ctctag 1496

<210> 94
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<223> Maize optimized CBHII

<400> 94
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aactggtccg gcccgacctg ctgcgcctcc ggctccacct gcgtgtactc caacgactac 120

tactcccagt gcctcccggg cgccgcctcc tcctcctcct ccacccgcgc cgcctccacc 180

acctcccgcg tgtccccgac cacctcccgc tcctcctccg ccaccccgcc gccgggctcc 240

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<212> DNA
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<223> Maize optimized EGLI

<400> 95
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<212> DNA
<213> Artificial Sequence

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<223> Maize optimized BGLII

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tag 2103

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acaagtaaca caatattaca aagttagttt catacaaagc aagaaaagga caataatact 180

tgacatgtaa agtgaagctt attatacttc ctaatccaac acaaaacaaa aaaaagttgc 240

acaaaggtcc aaaaatccac atcaaccatt aacctatacg taaagtgagt gatgagtcac 300

attatccaac aaatgtttat caatgtggta tcatacaagc attgacatcc cataaatgca 360

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<210> 99
<211> 1188

<212> DNA
<213> artificial sequence

<220>
<223> synthetic ferulic acid esterase

<400> 99
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ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc cacccgcccg 120

gcccgcgtgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180

ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg 240

atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaac 300

accaacgccg ccggcccggg catcgccgac ggctacgaga acttcaccaa ggacctcctc 360

aactccctca tcccgtacat cgagtccaac tactccgtgt acaccgaccg cgagcaccgc 420

gccatcgccg gcctctctat gggcggcggc cagtccttca acatcggcct caccaacctc 480

gacaagttcg cctacatcgg cccgatctcc gccgccccga acacctaccc gaacgagcgc 540

ctcttcccgg acggcggcaa ggccgcccgc gagaagctca agctcctctt catcgcctgc 600

ggcaccaacg actccctcat cggcttcggc cagcgcgtgc acgagtactg cgtggccaac 660

aacatcaacc acgtgtactg gctcatccag ggcggcggcc acgacttcaa cgtgtggaag 720

ccgggcctct ggaacttcct ccagatggcc gacgaggccg gcctcacccg cgacggcaac 780

accccggtgc cgaccccgtc cccgaagccg gccaacaccc gcatcgaggc cgaggactac 840

gacggcatca actcctcctc catcgagatc atcggcgtgc cgccggaggg cggccgcggc 900

atcggctaca tcacctccgg cgactacctc gtgtacaagt ccatcgactt cggcaacggc 960

gccacctcct tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc 1020

aacggcccga acggcaccct catcggcacc ctctccgtga agtccaccgg cgactggaac 1080

acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc 1140

gtgttcaagg gcccggtgaa catcgactgg ttcaccttcg gcgtgtag 1188

<210> 100
<211> 395
<212> PRT
<213> artificial sequence

<220>
<223> synthetic ferulic acid esterase

<400> 100

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Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
1               5                  10                  15

Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
            20                  25                  30

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
        35                  40                  45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
    50                  55                  60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
65                  70                  75                  80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
                85                  90                  95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
            100                 105                 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
        115                 120                 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
    130                 135                 140

Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
145                 150                 155                 160

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
                165                 170                 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
            180                 185                 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
        195                 200                 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
    210                 215                 220

Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
225                 230                 235                 240
```

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 101
<211> 1188
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13036

<400> 101
atggccgcct ccctcccgac catgccgccg tccggctacg accaggtgcg caacggcgtg 60

ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc cacccgcccg 120

gcccgcgtgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180

ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg 240

atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaac 300

accaacgccg ccggcccggg catcgccgac ggctacgaga acttcaccaa ggacctcctc 360

aactccctca tcccgtacat cgagtccaac tactccgtgt acaccgaccg cgagcaccgc 420

gccatcgccg gcctctctat gggcggcggc cagtccttca acatcggcct caccaacctc 480

gacaagttcg cctacatcgg cccgatctcc gccgccccga acacctaccc gaacgagcgc 540

ctcttcccgg acggcggcaa ggccgcccgc gagaagctca agctcctctt catcgcctgc 600

ggcaccaacg actccctcat cggcttcggc cagcgcgtgc acgagtactg cgtggccaac 660

aacatcaacc acgtgtactg gctcatccag ggcggcggcc acgacttcaa cgtgtggaag 720

ccgggcctct ggaacttcct ccagatggcc gacgaggccg gcctcacccg cgacggcaac 780

accccggtgc cgaccccgtc cccgaagccg gccaacaccc gcatcgaggc cgaggactac 840

gacggcatca actcctcctc catcgagatc atcggcgtgc cgccggaggg cggccgcggc 900

atcggctaca tcacctccgg cgactacctc gtgtacaagt ccatcgactt cggcaacggc 960

gccacctcct tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc 1020

aacggcccga acggcaccct catcggcacc ctctccgtga agtccaccgg cgactggaac 1080

acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc 1140

gtgttcaagg gcccggtgaa catcgactgg ttcaccttcg gcgtgtag 1188

<210> 102
<211> 395
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13036

<400> 102

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
1 5 10 15

Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
20 25 30

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
35 40 45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
65 70 75 80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
85 90 95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
100 105 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
115 120 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
130 135 140

Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
145 150 155 160

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
165 170 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
195 200 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
210 215 220

Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 103
<211> 1245
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13038

<400> 103
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gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120

cgcggccagg tggtgaacat ctcctacttc tccaccgcca ccaactccac ccgcccggcc 180

cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctcctc 240

cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300

gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 360

aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 420

tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480

atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 540

aagttcgcct acatcggccc gatctccgcc gccccgaaca cctacccgaa cgagcgcctc 600

ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcctgcggc 660

accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720

atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780

ggcctctgga acttcctcca gatggccgac gaggccggcc tcacccgcga cggcaacacc 840

ccggtgccga ccccgtcccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900

ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 960

ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020

acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080

ggcccgaacg gcaccctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1140

tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200

ttcaagggcc cggtgaacat cgactggttc accttcggcg tgtag 1245

<210> 104
<211> 414
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13038 aa

<400> 104

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85 90 95

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
405 410

<210> 105
<211> 1425
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13039

<400> 105
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gacgcgtcca cgttccgccg cggcgccgcg cagggcctga ggggggcccg ggcgtcggcg 120

gcggcggaca cgctcagcat gcggaccagc gcgcgcgcgg cgcccaggca ccagcaccag 180

caggcgcgcc gcggggccag gttcccgtcg ctcgtcgtgt gcgccagcgc cggcgccatg 240

gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 300

cgcggccagg tggtgaacat ctcctacttc tccaccgcca ccaactccac ccgcccggcc 360

cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctcctc 420

cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 480

gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 540

aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 600

tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 660

atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 720

aagttcgcct acatcggccc gatctccgcc gccccgaaca cctacccgaa cgagcgcctc 780

ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcctgcggc 840

accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 900

atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 960

ggcctctgga acttcctcca gatggccgac gaggccggcc tcacccgcga cggcaacacc 1020

ccggtgccga ccccgtcccc gaagccggcc aacacccgca tcgaggccga ggactacgac 1080

ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 1140

ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1200

acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1260

ggcccgaacg gcaccctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1320

tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1380

ttcaagggcc cggtgaacat cgactggttc accttcggcg tgtag 1425

<210> 106
<211> 474
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13039 aa

<400> 106

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1 5 10 15

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20 25 30

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35 40 45

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50 55 60

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65 70 75 80

Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val Arg
85 90 95

Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser Thr
100 105 110

Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly Tyr
115 120 125

Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile Gly
130 135 140

Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val Ile
145 150 155 160

Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile Val
165 170 175

Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr Glu
180 185 190

Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu Ser
195 200 205

Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly Leu
210 215 220

Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu Asp
225 230 235 240

Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr Pro
245 250 255

Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys Leu
260 265 270

Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly Phe
275 280 285

Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His Val
290 295 300

Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys Pro
305 310 315 320

Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr Arg
325 330 335

Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn Thr
340 345 350

Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile Glu
355 360 365

Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile Thr
370 375 380

Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly Ala
385 390 395 400

Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile Glu
405 410 415

Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser Val
420 425 430

Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser Ile
435 440 445

Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly Pro
450 455 460

Val Asn Ile Asp Trp Phe Thr Phe Gly Val
465 470

<210> 107
<211> 1263
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13347

<400> 107
atgagggtgt tgctcgttgc cctcgctctc ctggctctcg ctgcgagcgc cacctccatg 60

gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120

cgcggccagg tggtgaacat ctcctacttc tccaccgcca ccaactccac ccgcccggcc 180

cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctcctc 240

cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300

gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 360

aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 420

tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480

atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 540

aagttcgcct acatcggccc gatctccgcc gccccgaaca cctacccgaa cgagcgcctc 600

ttcccggacg gcggcaaggc cgcccgcgag aagctcaagc tcctcttcat cgcctgcggc 660

accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720

atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780

ggcctctgga acttcctcca gatggccgac gaggccggcc tcacccgcga cggcaacacc 840

ccggtgccga ccccgtcccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900

ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 960

ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020

acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080

ggcccgaacg gcaccctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1140

tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200

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tag 1263

<210> 108
<211> 420
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13347

<400> 108

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

```
His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
                85                  90                  95

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
            100                 105                 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
        115                 120                 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
    130                 135                 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
145                 150                 155                 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
                165                 170                 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
            180                 185                 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
        195                 200                 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
    210                 215                 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
225                 230                 235                 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
                245                 250                 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
            260                 265                 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
        275                 280                 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
    290                 295                 300
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Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Ser Glu
405 410 415

Lys Asp Glu Leu
420

<210> 109
<211> 1296
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 11267

<400> 109
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gcgcagtccg agccggagct gaagctggag tccgtggtga tcgtgtcccg ccacggcgtg 120

cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccggacgc ctggccgacc 180

tggccggtga agctcggcga gctgaccccg cgcggcggcg agctgatcgc ctacctcggc 240

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<223> plasmid 11267 aa sequence

<400> 110

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
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Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65 70 75 80

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His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
                85                  90                  95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
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Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
        115                 120                 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
    130                 135                 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
145                 150                 155                 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
                165                 170                 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
            180                 185                 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
        195                 200                 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
    210                 215                 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225                 230                 235                 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
                245                 250                 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
            260                 265                 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
        275                 280                 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
    290                 295                 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305                 310                 315                 320
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Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
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Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
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<212> DNA
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cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccggacgc ctggccgacc 180

tggccggtga agctcggcga gctgaccccg cgcggcggcg agctgatcgc ctacctcggc 240

cactactggc gccagcgcct cgtggccgac ggcctcctcc cgaagtgcgg ctgcccgcag 300

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gccggctgcg aggagcgcaa cgcccagggc atgtgctccc tcgccggctt cacccagatc 1260

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<212> PRT
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<220>
<223> plasmid 11268 amino acid sequence

<400> 112

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
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Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20 25 30

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35 40 45

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50 55 60

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65 70 75 80

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Ser
420 425 430

Glu Lys Asp Glu Leu
435